(19) Europäisches Patentamt
European Patent Office
Office européen des brevets

(11) EP 1 130 094 A2

(12) EUROPEAN PATENT APPLICATION

(43) Date of publication:
05.09.2001 Bulletin 2001/36

(21) Application number: **00114089.6**

(22) Date of filing: **07.07.2000**

(51) Int Cl.[7]: **C12N 15/12**, C12N 15/11, C12N 15/10, C12N 15/70, C12N 15/85, C12N 5/10, C12N 1/21, C07K 14/47, C07K 16/18, C12Q 1/68

(84) Designated Contracting States:
AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
Designated Extension States:
AL LT LV MK RO SI

(30) Priority: **08.07.1999 JP 19448699**
11.01.2000 JP 2000118774
02.05.2000 JP 2000183765

(71) Applicant: **Helix Research Institute**
Kisarazu-shi, Chiba 292-0812 (JP)

(72) Inventors:
- **Ota, Toshio**
  Fujisawa-shi, Kanagawa 251-0042 (JP)
- **Nishikawa, Tetsuo**
  Tokyo 173-0013 (JP)
- **Isogai, Takao**
  Inashiki-gun, Ibaraki 300-0303 (JP)
- **Hayashi, Koji**
  Ichihara-shi, Chiba 299-0125 (JP)
- **Ishii, Shizuko**
  Kisarazu-shi, Chiba 292-0812 (JP)
- **Kawai, Yuri**
  Kisarazu-shi, Chiba 292-0812 (JP)
- **Wakamatsu, Ai**
  Kisarazu-shi, Chiba 292-0014 (JP)
- **Sugiyama, Tomoyasu**
  Kisarazu-shi, Chiba 292-0045 (JP)
- **Nagai, Keiichi**
  Higashiyamato-shi, Tokyo 207-0022 (JP)
- **Kojima, Shinichi**
  Kisarazu-shi, Chiba 292-0052 (JP)
- **Otsuki, Tetsuji**
  Kisarazu-shi, Chiba 292-0055 (JP)
- **Koga, Hisashi**
  Kisarazu-shi, Chiba 292-0055 (JP)

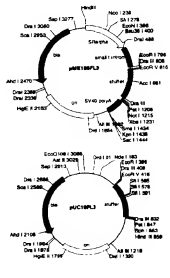
(74) Representative: **VOSSIUS & PARTNER**
Siebertstrasse 4
81675 München (DE)

Remarks:
The sequence listing, which is published as annex to the application documents, was filed after the date of filing. The applicant has declared that it does not include matter which goes beyond the content of the application as filed.

(54) Primers for synthesizing full length cDNA clones and their use

(57) Primers for synthesizing full length cDNAs and their use are provided.

830 cDNA encoding a human protein has been isolated and nucleotide sequences of 5'-, and 3'-ends of the cDNA have been determined. Furthermore, primers for synthesizing the full length cDNA have been provided to clarify the function of the protein encoded by the cDNA. The full length cDNA of the present invention containing the translation start site provides information useful for analyzing the functions of the protein.



EP 1 130 094 A2

Description

FIELD OF THE INVENTION

[0001] The present invention relates to a polynucleotide encoding a novel protein, a protein encoded by the polynucleotide, and new uses of these.

BACKGROUND OF THE INVENTION

[0002] Currently, the sequencing projects, the determination and analysis of the genomic DNA of various living organisms have been in progress all over the world. The whole genomic sequences of more than 10 species of prokaryotes, a lower eukaryote, yeast, and a multicellular eukaryote, C. elegans are already determined. As to human genome, which is supposed to be composed of three thousand million base pairs, the world wide cooperative projects have been under way to analyze it, and the whole structure is predicted to be determined by the years 2002-2003. The aim of the determination of genomic sequence is to reveal the functions of all genes and their regulation and to understand living organisms as a network of interactions between genes, proteins, cells or individuals through deducing the information in a genome, which is a blueprint of the highly complicated living organisms. To understand living organisms by utilizing the genomic information from various species is not only important as an academic subject, but also socially significant from the viewpoint of industrial application.

[0003] However, determination of genomic sequences itself cannnot identify the functions of all genes. For example, as for yeast, only the function of approximately half of the 6000 genes, which is predicted based on the genomic sequence, was able to be deduced. As for human, the number of the genes is predicted to be approximately one hundred thousand. Therefore, it is desirable to establish "a high throughput analysis system of the gene functions" which allows us to identify rapidly and efficiently the functions of vast amounts of the genes obtained by the genomic sequencing.

[0004] Many genes in the eukaryotic genome are split by introns into multiple exons. Thus, it is difficult to predict correctly the structure of encoded protein solely based on genomic information. In contrast, cDNA, which is produced from mRNA that lacks introns, encodes a protein as a single continuous amino acid sequence and allows us to identify the primary structure of the protein easily. In human cDNA research, to date, more than one million ESTs (Expression Sequence Tags) are publicly available, and the ESTs presumably cover not less than 80% of all human genes.

[0005] The information of ESTs is utilized for analyzing the structure of human genome, or for predicting the exon-regions of genomic sequences or their expression profile. However, many human ESTs have been derived from proximal regions to the 3'-end of cDNA, and information around the 5'-end of mRNA is extremely little. Among these human cDNAs, the number of the corresponding mRNAs whose encoding protein sequences are deduced is approximately 7000, and further, the number of full-length therein is only 5500. Thus, even including cDNA registered as EST, the percentage of human cDNA obtained so far is estimated to be 10-15% of all the genes.

[0006] It is possible to identify the transcription start site of mRNA on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA that is contained in the cDNA, or in its regulation of expression at the translation stage. Also, since a full-length cDNA contains ATG, the translation start site, in the 5'-region, it can be translated into a protein in a correct frame. Therefore, it is possible to produce a large amount of the protein encoded by the cDNA or to analyze biological activity of the expressed protein by utilizing an appropriate expression system. Thus, analysis of a full-length cDNA provides valuable information which complements the information from genome sequencing. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

[0007] In particular, human secretory proteins or membrane proteins are would be useful by itself as a medicine like tissue plasminogen activator (TPA), or as a target of medicines like membrane receptors. In addition, genes for signal transduction-associated proteins (protein kinases, etc.), glycoprotein-associated proteins, transcription-associated proteins, and disease-associated proteins form a gene group rich in genes whose relationships to human diseases have been elucidated.

[0008] Therefore, it has great significance to isolate novel full-length cDNA clones of human, only few of which has been isolated. Especially, isolation of a novel cDNA clone encoding a secretory protein or membrane protein is desired since the protein itself would be useful as a medicine, and also the clones potentially include a gene associated with diseases. In addition, genes encoding proteins that are associated with signal transduction, glycoprotein, transcription, or diseases are expected to be useful as target molecules for therapy, or as medicines themselves. These genes form a gene group predicted to be strongly associated with diseases. Thus, identification of the full-length cDNA clones encoding those proteins has great significance.

SUMMARY OF THE INVENTION

[0009] An objective of the present invention is to provide a primer that enables synthesizing polynucleotide from human, the resulting polynucleotide or its clone, and a protein encoded by the polynucleotide.

[0010] The inventors have developed a method for efficiently cloning a human full-length cDNA that is predicted by the ATGpr etc. to be a full-length cDNA clone, from a full-length-enriched cDNA library that is synthesized by the oligo-capping method. Then, the inventors determined the nucleotide sequence of the obtained cDNA clones from both 5'- and 3'- ends. By utilizing the sequences, the inventors selected clones that were expected to contain a signal by the PSORT (Nakai K. and Kanehisa M. (1992) Genomics 14: 897-911), and obtained clones that contain a cDNA encoding a secretory protein or membrane protein. Moreover, the inventors specifically selected full-length cDNA clones that encode secretory or membrane proteins, signal transduction-associated proteins, glycoprotein-associated proteins, transcription-associated proteins, or disease-associated proteins from clones homologous to the clones in the Swiss-Prot (http://www.ebi.ac.uk/ebi_docsSwissProt_db/swisshome.html) according to the keywords of SwissProt.

[0011] The full-length cDNA clones of the present invention have high fullness ratio since these were obtained by the combination of (1) construction of a full-length-enriched cDNA library that is synthesized by the oligo-capping method, and (2) a system in which fullness ratio is evaluated from the nucleotide sequence of the 5'-end (in this system, clones are selected based on the estimation by the ATGpr, following the removal of sequences judged not to be full-length when compared with ESTs). However, the primers of the present invention enable obtaining full-length cDNA easily without any special methods mentioned above.

[0012] Homology analysis in which the analysis is carried out against a non-full-length cDNA fragment to postulate the function of a protein encoded by said fragment, is being commonly performed. However, since such analysis is based on the information of the fragment, it is not clear as to whether this fragment corresponds to a part that is functionally important in the protein. In other words, the reliability of the homology analysis based on the information of a fragment is doubtful, as information relating to the structure of the whole protein is not available. However, the homology analysis of the present invention is conducted based on the information of a full-length cDNA comprising the whole coding region of the cDNA, and therefore, the homology of various portions of the protein can be analyzed. Hence, the reliability of the homology analysis has been dramatically improved in the present invention.

[0013] The inventors completed the invention by finding that it is possible to synthesize a novel full-length cDNA by using the combination of a primer that is designed based on the nucleotide sequence of the 5'-ends of the selected full-length cDNA clones and any of an oligo-dT primer or a 3'-primer that is designed based on the nucleotide sequence of the 3'-ends of the selected clones.

[0014] Thus, the present invention relates to primers described below, a method for synthesizing a polynucleotide using the primers, and polynucleotides obtained by the method.

[0015] First, the present invention relates to

(1) use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides;

(2) a primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, wherein said oligonucleotide comprises at least 15 nucleotides; and

(3) A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nuclectide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence / 3'-end nucleotide sequence is selected from the combinations of 5'-end nucleotide sequence / 3'-end nucleotide sequence set forth in the SEQ ID NOs in Table 1.

[0016] Table 1 shows names of clones obtained in the examples described later, comprising the polynucleotide of the present invention (830 clones), names of nucleotide sequences at the 5'-end and 3'-end of the full-length cDNA, and their corresponding SEQ ID NOs. A blank indicates that the of the 3'-end sequence corresponding to the 5'-end sequence has not been determined the same clone.

[0017] The SEQ ID NO of a 5'-end sequence is shown on the right side of the name of the 5'-end sequence, and the SEQ ID NO of a 3'-end sequence is shown on the right side of the name of the 3'-end sequence.

Table 1

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
BNGH41000020	F-BNGH41000020	1		
BNGH41000087	F-BNGH41000087	2		
BNGH41000091	F-BNGH41000091	3		
HEMBA1000006	F-HEMBA1000006	4	R-HEMBA1000006	830
HEMBA1000121	F-HEMBA1000121	5	R-HEMBA1000121	831
HEMBA1000128	F-HEMBA1000128	6	R-HEMBA1000128	832
HEMBA1000275	F-HEMBA1000275	7	R-HEMBA1000275	833
HEMBA1000300	F-HEMBA1000300	8	R-HEMBA1000300	834
HEMBA1000349	F-HEMBA1000349	9	R-nnnnnnnnnnn	835
HEMBA1000443	F-HEMBA1000443	10		
HEMBA1000462	F-HEMBA1000462	11	R-HEMBA1000462	836
HEMBA1000477	F-HEMBA1000477	12	R-HEMBA1000477	837
HEMBA1000590	F-HEMBA1000590	13	R-HEMBA1000590	838
HEMBA1000634	F-HEMBA1000634	14	R-HEMBA1000634	839
HEMBA1000671	F-HEMBA1000671	15	R-HEMBA1000671	840
HEMBA1000713	F-HEMBA1000713	16	R-HEMBA1000713	841
HEMBA1000732	F-HEMBA1000732	17	R-HEMBA1000732	842
HEMBA1000745	F-HEMBA1000745	18	R-nnnnnnnnnnn	843
HEMBA1000835	F-HEMBA1000835	19		
HEMBA1000875	F-HEMBA1000875	20	R-HEMBA1000875	844
HEMBA1000907	F-HEMBA1000907	21		
HEMBA1000940	F-HEMBA1000940	22	R-HEMBA1000940	845
HEMBA1000962	F-HEMBA1000962	23	R-HEMBA1000962	846
HEMBA1001184	F-HEMBA1001184	24	R-HEMBA1001184	847
HEMBA1001221	F-HEMBA1001221	25	R-HEMBA1001221	848
HEMBA1001228	F-HEMBA1001228	26	R-HEMBA1001228	849
HEMBA1001272	F-HEMBA1001272	27	R-HEMBA1001272	850
HEMBA1001296	F-HEMBA1001296	28	R-HEMBA1001296	851
HEMBA1001297	F-HEMBA1001297	29	R-HEMBA1001297	852
HEMBA1001390	F-HEMBA1001390	30	R-HEMBA1001390	853
HEMBA1001563	F-HEMBA1001563	31	R-HEMBA1001563	854
HEMBA1001621	F-HEMBA1001621	32	R-HEMBA1001621	855
HEMBA1001878	F-HEMBA1001878	33	R-HEMBA1001878	856
HEMBA1001886	F-HEMBA1001886	34	R-HEMBA1001886	857
HEMBA1002048	F-HEMBA1002048	35	R-HEMBA1002048	858
HEMBA1002131	F-HEMBA1002131	36	R-HEMBA1002131	859
HEMBA1002163	F-HEMBA1002163	37	R-HEMBA1002163	860
HEMBA1002164	F-HEMBA1002164	38		
HEMBA1002167	F-HEMBA1002167	39	R-HEMBA1002167	861
HEMBA1002178	F-HEMBA1002178	40	R-HEMBA1002178	862
HEMBA1002195	F-HEMBA1002195	41	R-HEMBA1002195	863
HEMBA1002227	F-HEMBA1002227	42	R-HEMBA1002227	864
HEMBA1002239	F-HEMBA1002239	43		
HEMBA1002316	F-HEMBA1002316	44	R-HEMBA1002316	865
HEMBA1002420	F-HEMBA1002420	45	R-HEMBA1002420	866
HEMBA1002421	F-HEMBA1002421	46	R-HEMBA1002421	867
HEMBA1002524	F-HEMBA1002524	47	R-HEMBA1002524	868

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
HEMBA1002551	F-HEMBA1002551	48	R-HEMBA1002551	869
HEMBA1002767	F-HEMBA1002767	49	R-HEMBA1002767	870
HEMBA1002985	F-HEMBA1002985	50	R-HEMBA1002985	871
HEMBA1002992	F-HEMBA1002992	51		
HEMBA1003047	F-HEMBA1003047	52	R-HEMBA1003047	872
HEMBA1003072	F-HEMBA1003072	53	R-HEMBA1003072	873
HEMBA1003101	F-HEMBA1003101	54	R-HEMBA1003101	874
HEMBA1003120	F-HEMBA1003120	55	R-HEMBA1003120	875
HEMBA1003230	F-HEMBA1003230	56	R-HEMBA1003230	876
HEMBA1003294	F-HEMBA1003294	57	R-HEMBA1003294	877
HEMBA1003315	F-HEMBA1003315	58	R-HEMBA1003315	878
HEMBA1003392	F-HEMBA1003392	59	R-HEMBA1003392	879
HEMBA1003399	F-HEMBA1003399	60	R-HEMBA1003399	880
HEMBA1003487	F-HEMBA1003487	61	R-HEMBA1003487	881
HEMBA1003497	F-HEMBA1003497	62	R-HEMBA1003497	882
HEMBA1003530	F-HEMBA1003530	63	R-HEMBA1003530	883
HEMBA1003602	F-HEMBA1003602	64	R-HEMBA1003602	884
HEMBA1003732	F-HEMBA1003732	65	R-HEMBA1003732	885
HEMBA1003945	F-HEMBA1003945	66	R-HEMBA1003945	886
HEMBA1004007	F-HEMBA1004007	67	R-HEMBA1004007	887
HEMBA1004067	F-HEMBA1004067	68		
HEMBA1004085	F-HEMBA1004085	69	R-HEMBA1004085	888
HEMBA1004110	F-HEMBA1004110	70	R-nnnnnnnnnnn	889
HEMBA1004250	F-HEMBA1004250	71	R-HEMBA1004250	890
HEMBA1004391	F-HEMBA1004391	72	R-HEMBA1004391	891
HEMBA1004444	F-HEMBA1004444	73	R-HEMBA1004444	892
HEMBA1004454	F-HEMBA1004454	74	R-HEMBA1004454	893
HEMBA1004505	F-HEMBA1004505	75	R-HEMBA1004505	894
HEMBA1004785	F-HEMBA1004785	76	R-HEMBA1004785	895
HEMBA1004797	F-HEMBA1004797	77	R-HEMBA1004797	896
HEMBA1004952	F-HEMBA1004952	78	R-HEMBA1004952	897
HEMBA1004971	F-HEMBA1004971	79	R-HEMBA1004971	898
HEMBA1004982	F-HEMBA1004982	80	R-HEMBA1004982	899
HEMBA1005070	F-HEMBA1005070	81	R-HEMBA1005070	900
HEMBA1005084	F-HEMBA1005084	82	R-HEMBA1005084	901
HEMBA1005145	F-HEMBA1005145	83	R-HEMBA1005145	902
HEMBA1005230	F-HEMBA1005230	84	R-HEMBA1005230	903
HEMBA1005246	F-HEMBA1005246	85	R-HEMBA1005246	904
HEMBA1005267	F-HEMBA1005267	86	R-HEMBA1005267	905
HEMBA1005337	F-HEMBA1005337	87	R-HEMBA1005337	906
HEMBA1005430	F-HEMBA1005430	88	R-HEMBA1005430	907
HEMBA1005449	F-HEMBA1005449	89	R-HEMBA1005449	908
HEMBA1005489	F-HEMBA1005489	90	R-HEMBA1005489	909
HEMBA1005522	F-HEMBA1005522	91	R-HEMBA1005522	910
HEMBA1005545	F-HEMBA1005545	92	R-HEMBA1005545	911
HEMBA1005698	F-HEMBA1005698	93	R-HEMBA1005698	912
HEMBA1005913	F-HEMBA1005913	94	R-HEMBA1005913	913
HEMBA1005929	F-HEMBA1005929	95	R-HEMBA1005929	914

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
HEMBA1005945	F-HEMBA1005945	96	R-HEMBA1005945	915
HEMBA1006016	F-HEMBA1006016	97	R-HEMBA1006016	916
HEMBA1006171	F-HEMBA1006171	98	R-HEMBA1006171	917
HEMBA1006276	F-HEMBA1006276	99	R-HEMBA1006276	918
HEMBA1006299	F-HEMBA1006299	100	R-HEMBA1006299	919
HEMBA1006311	F-HEMBA1006311	101	R-HEMBA1006311	920
HEMBA1006335	F-HEMBA1006335	102	R-HEMBA1006335	921
HEMBA1006357	F-HEMBA1006357	103	R-HEMBA1006357	922
HEMBA1006430	F-HEMBA1006430	104	R-HEMBA1006430	923
HEMBA1006482	F-HEMBA1006482	105	R-HEMBA1006482	924
HEMBA1006517	F-HEMBA1006517	106	R-HEMBA1006517	925
HEMBA1006544	F-HEMBA1006544	107	R-HEMBA1006544	926
HEMBA1006572	F-HEMBA1006572	108	R-HEMBA1006572	927
HEMBA1006658	F-HEMBA1006658	109	R-HEMBA1006658	928
HEMBA1006707	F-HEMBA1006707	110	R-HEMBA1006707	929
HEMBA1006724	F-HEMBA1006724	111	R-HEMBA1006724	930
HEMBA1006749	F-HEMBA1006749	112	R-HEMBA1006749	931
HEMBA1006770	F-HEMBA1006770	113	R-HEMBA1006770	932
HEMBA1006902	F-HEMBA1006902	114	R-HEMBA1006902	933
HEMBA1006912	F-HEMBA1006912	115	R-HEMBA1006912	934
HEMBA1006916	F-HEMBA1006916	116	R-HEMBA1006916	935
HEMBA1006960	F-HEMBA1006960	117	R-HEMBA1006960	936
HEMBA1007013	F-HEMBA1007013	118	R-HEMBA1007013	937
HEMBA1007057	F-HEMBA1007057	119	R-HEMBA1007057	938
HEMBA1007063	F-HEMBA1007063	120	R-HEMBA1007063	939
HEMBA1007226	F-HEMBA1007226	121		
HEMBA1007241	F-HEMBA1007241	122	R-HEMBA1007241	940
HEMBA1007291	F-HEMBA1007291	123	R-HEMBA1007291	941
HEMBA1007332	F-HEMBA1007332	124	R-HEMBA1007332	942
HEMBB1000106	F-HEMBB1000106	125	R-HEMBB1000106	943
HEMBB1000276	F-HEMBB1000276	126	R-HEMBB1000276	944
HEMBB1000309	F-HEMBB1000309	127	R-HEMBB1000309	945
HEMBB1000407	F-HEMBB1000407	128	R-HEMBB1000407	946
HEMBB1000447	F-HEMBB1000447	129	R-HEMBB1000447	947
HEMBB1000542	F-HEMBB1000542	130	R-HEMBB1000542	948
HEMBB1000567	F-HEMBB1000567	131	R-HEMBB1000567	949
HEMBB1000642	F-HEMBB1000642	132	R-HEMBB1000642	950
HEMBB1000668	F-HEMBB1000668	133	R-HEMBB1000668	951
HEMBB1000679	F-HEMBB1000679	134	R-HEMBB1000679	952
HEMBB1000881	F-HEMBB1000881	135	R-HEMBB1000881	953
HEMBB1000905	F-HEMBB1000905	136	R-HEMBB1000905	954
HEMBB1001026	F-HEMBB1001026	137	R-HEMBB1001026	955
HEMBB1001048	F-HEMBB1001048	138	R-HEMBB1001048	956
HEMBB1001200	F-HEMBB1001200	139	R-HEMBB1001200	957
HEMBB1001407	F-HEMBB1001407	140	R-HEMBB1001407	958
HEMBB1001530	F-HEMBB1001530	141	R-HEMBB1001530	959
HEMBB1001547	F-HEMBB1001547	142	R-HEMBB1001547	960
HEMBB1001573	F-HEMBB1001573	143	R-HEMBB1001573	961

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
HEMBB1001847	F-HEMBB1001847	144	R-HEMBB1001847	962
HEMBB1001959	F-HEMBB1001959	145	R-HEMBB1001959	963
HEMBB1001978	F-HEMBB1001978	146	R-HEMBB1001978	964
HEMBB1002039	F-HEMBB1002039	147	R-HEMBB1002039	965
HEMBB1002041	F-HEMBB1002041	148	R-HEMBB1002041	966
HEMBB1002051	F-HEMBB1002051	149	R-HEMBB1002051	967
HEMBB1002120	F-HEMBB1002120	150	R-HEMBB1002120	968
HEMBB1002162	F-HEMBB1002162	151	R-HEMBB1002162	969
HEMBB1002228	F-HEMBB1002228	152	R-HEMBB1002228	970
HEMBB1002245	F-HEMBB1002245	153	R-HEMBB1002245	971
HEMBB1002302	F-HEMBB1002302	154	R-HEMBB1002302	972
HEMBB1002427	F-HEMBB1002427	155	R-HEMBB1002427	973
HEMBB1002465	F-HEMBB1002465	156	R-HEMBB1002465	974
HEMBB1002661	F-HEMBB1002661	157	R-HEMBB1002661	975
HEMBB1002663	F-HEMBB1002663	158	R-HEMBB1002663	976
HEMBB1002693	F-HEMBB1002693	159	R-HEMBB1002693	977
MAMMA 1000046	F-MAMMA1000046	160	R-MAMMA1000046	978
MAMMA1000102	F-MAMMA1000102	161	R-MAMMA1000102	979
MAMMA 1000106	F-MAMMA1000106	162	R-MAMMA1000106	980
MAMMA1000118	F-MAMMA1000118	163	R-MAMMA1000118	981
MAMMA1000141	F-MAMMA1000141	164	R-MAMMA1000141	982
MAMMA1000204	F-MAMMA1000204	165	R-MAMMA1000204	983
MAMMA1000226	F-MAMMA1000226	166	R-MAMMA1000226	984
MAMMA1000403	F-MAMMA1000403	167	R-MAMMA1000403	985
MAMMA1000449	F-MAMMA1000449	168	R-MAMMA1000449	986
MAMMA1000457	F-MAMMA1000457	169	R-MAMMA1000457	987
MAMMA1000473	F-MAMMA1000473	170	R-MAMMA1000473	988
MAMMA1000496	F-MAMMA1000496	171	R-MAMMA1000496	989
MAMMA1000528	F-MAMMA1000528	172	R-MAMMA1000528	990
MAMMA1000591	F-MAMMA1000591	173	R-MAMMA1000591	991
MAMMA 1000614	F-MAMMA1000614	174	R-MAMMA1000614	992
MAMMA1000652	F-MAMMA1000652	175	R-MAMMA1000652	993
MAMMA1000681	F-MAMMA1000681	176	R-MAMMA1000681	994
MAMMA 1000706	F-MAMMA1000706	177	R-MAMMA1000706	995
MAMMA 1000788	F-MAMMA1000788	178	R-MAMMA1000788	996
MAMMA 1000810	F-MAMMA1000810	179	R-MAMMA1000810	997
MAMMA1000814	F-MAMMA1000814	180	R-MAMMA1000814	998
MAMMA1000881	F-MAMMA1000881	181	R-MAMMA1000881	999
MAMMA1000986	F-MAMMA1000986	182	R-MAMMA1000986	1000
MAMMA 1000994	F-MAMMA1000994	183	R-MAMMA1000994	1001
MAMMA1001043	F-MAMMA1001043	184	R-MAMMA1001043	1002
MAMMA1001066	F-MAMMA1001066	185	R-MAMMA1001066	1003
MAMMA1001094	F-MAMMA1001094	186	R-MAMMA1001094	1004
MAMMA1001141	F-MAMMA1001141	187	R-MAMMA1001141	1005
MAMMA1001150	F-MAMMA1001150	188	R-MAMMA1001150	1006
MAMMA1001237	F-MAMMA1001237	189	R-MAMMA1001237	1007
MAMMA1001284	F-MAMMA1001284	190	R-MAMMA1001284	1008
MAMMA1001310	F-MAMMA1001310	191	R-MAMMA1001310	1009

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
MAMMA1001344	F-MAMMA1001344	192		
MAMMA1001418	F-MAMMA1001418	193	R-MAMMA1001418	1010
MAMMA1001532	F-MAMMA1001532	194	R-MAMMA1001532	1011
MAMMA1001609	F-MAMMA1001609	195	R-MAMMA1001609	1012
MAMMA 1001615	F-MAMMA1001615	196	R-MAMMA1001615	1013
MAMMA 1001623	F-MAMMA1001623	197	R-MAMMA1001623	1014
MAMMA1001634	F-MAMMA1001634	198	R-MAMMA1001634	1015
MAMMA 1001893	F-MAMMA1001893	199	R-MAMMA1001893	1016
MAMMA1001901	F-MAMMA1001901	200	R-MAMMA1001901	1017
MAMMA 1001957	F-MAMMA1001957	201	R-MAMMA1001957	1018
MAMMA1001978	F-MAMMA1001978	202	R-MAMMA1001978	1019
MAMMA1002070	F-MAMMA1002070	203	R-MAMMA1002070	1020
MAMMA1002080	F-MAMMA1002080	204	R-MAMMA1002080	1021
MAMMA 1002087	F-MAMMA1002087	205	R-MAMMA1002087	1022
MAMMA1002091	F-MAMMA1002091	206		
MAMMA 1002095	F-MAMMA1002095	207	R-MAMMA1002095	1023
MAMMA 1002128	F-MAMMA1002128	208	R-MAMMA1002128	1024
MAMMA1002142	F-MAMMA1002142	209	R-MAMMA1002142	1025
MAMMA1002165	F-MAMMA1002165	210	R-MAMMA1002165	1026
MAMMA 1002205	F-MAMMA1002205	211	R-MAMMA1002205	1027
MAMMA 1002224	F-MAMMA1002224	212	R-MAMMA1002224	1028
MAMMA1002234	F-MAMMA1002234	213	R-MAMMA1002234	1029
MAMMA1002586	F-MAMMA1002586	214	R-MAMMA1002586	1030
MAMMA1002633	F-MAMMA1002633	215	R-MAMMA1002633	1031
MAMMA1003126	F-MAMMA1003126	216	R-MAMMA1003126	1032
NT2RM1000407	F-NT2RM1000407	217		
NT2RM1000462	F-NT2RM1000462	218		
NT2RM1000542	F-NT2RM1000542	219		
NT2RM1000580	F-NT2RM1000580	220		
NT2RM1000789	F-NT2RM1000789	221		
NT2RM1000855	F-NT2RM1000855	222		
NT2RM1000858	F-NT2RM1000858	223		
NT2RM1000899	F-NT2RM1000899	224		
NT2RM2000241	F-NT2RM2000241	225		
NT2RM2000306	F-NT2RM2000306	226		
NT2RM2000410	F-NT2RM2000410	227		
NT2RM2000423	F-NT2RM2000423	228		
NT2RM2000497	F-NT2RM2000497	229		
NT2RM2000514	F-NT2RM2000514	230		
NT2RM2000565	F-NT2RM2000565	231		
NT2RM2000582	F-NT2RM2000582	232		
NT2RM2000589	F-NT2RM2000589	233		
NT2RM2000622	F-NT2RM2000622	234		
NT2RM2000632	F-NT2RM2000632	235		
NT2RM2000773	F-NT2RM2000773	236		
NT2RM2001126	F-NT2RM2001126	237		
NT2RM2001558	F-NT2RM2001558	238		
NT2RM2001626	F-NT2RM2001626	239		

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RM2001643	F-NT2RM2001643	240		
NT2RM2001738	F-NT2RM2001738	241		
NT2RM2001767	F-NT2RM2001767	242		
NT2RM2001792	F-NT2RM2001792	243		
NT2RM2001818	F-NT2RM2001818	244		
NT2RM2001902	F-NT2RM2001902	245		
NT2RM2001939	F-NT2RM2001939	246		
NT2RM2001941	F-NT2RM2001941	247		
NT2RM4000100	F-NT2RM4000100	248	R-NT2RM4000100	1033
NT2RM4000115	F-NT2RM4000115	249	R-NT2RM4000115	1034
NT2RM4000198	F-NT2RM4000198	250	R-NT2RM4000198	1035
NT2RM4000284	F-NT2RM4000284	251	R-NT2RM4000284	1036
NT2RM4000295	F-NT2RM4000295	252	R-NT2RM4000295	1037
NT2RM4000326	F-NT2RM4000326	253	R-NT2RM4000326	1038
NT2RM4000417	F-NT2RM4000417	254	R-NT2RM4000417	1039
NT2RM4000444	F-NT2RM4000444	255	R-NT2RM4000444	1040
NT2RM4000587	F-NT2RM4000587	256	R-NT2RM4000587	1041
NT2RM4000593	F-NT2RM4000593	257	R-NT2RM4000593	1042
NT2RM4000648	F-NT2RM4000648	258	R-NT2RM4000648	1043
NT2RM4000761	F-NT2RM4000761	259	R-NT2RM4000761	1044
NT2RM4000965	F-NT2RM4000965	260	R-NT2RM4000965	1045
NT2RM4000997	F-NT2RM4000997	261	R-NT2RM4000997	1046
NT2RM4001321	F-NT2RM4001321	262	R-NT2RM4001321	1047
NT2RM4001325	F-NT2RM4001325	263	R-NT2RM4001325	1048
NT2RM4001377	F-NT2RM4001377	264	R-NT2RM4001377	1049
NT2RM4001735	F-NT2RM4001735	265	R-NT2RM4001735	1050
NT2RM4001768	F-NT2RM4001768	266	R-NT2RM4001768	1051
NT2RM4001843	F-NT2RM4001843	267	R-NT2RM4001843	1052
NT2RM4002352	F-NT2RM4002352	268	R-NT2RM4002352	1053
NT2RP1000002	F-NT2RP1000002	269		
NT2RP1000050	F-NT2RP1000050	270		
NT2RP1000181	F-NT2RP1000181	271		
NT2RP1000239	F-NT2RP1000239	272		
NT2RP1000261	F-NT2RP1000261	273		
NT2RP1000271	F-NT2RP1000271	274		
NT2RP1000300	F-NT2RP1000300	275		
NT2RP1000325	F-NT2RP1000325	276		
NT2RP1000448	F-NT2RP1000448	277		
NT2RP1000465	F-NT2RP1000465	278		
NT2RP1000468	F-NT2RP1000468	279		
NT2RP1000551	F-NT2RP1000551	280		
NT2RP1000579	F-NT2RP1000579	281		
NT2RP1000613	F-NT2RP1000613	282		
NT2RP1000679	F-NT2RP1000679	283		
NT2RP1000740	F-NT2RP1000740	284		
NT2RP1000903	F-NT2RP1000903	285		
NT2RP1000981	F-NT2RP1000981	286		
NT2RP1001004	F-NT2RP1001004	287		

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RP1001020	F-NT2RP1001020	288		
NT2RP1001031	F-NT2RP1001031	289		
NT2RP1001563	F-NT2RP1001563	290		
NT2RP2000092	F-NT2RP2000092	291	R-NT2RP2000092	1054
NT2RP2000178	F-NT2RP2000178	292	R-NT2RP2000178	1055
NT2RP2000240	F-NT2RP2000240	293	R-NT2RP2000240	1056
NT2RP2000394	F-NT2RP2000394	294	R-NT2RP2000394	1057
NT2RP2000447	F-NT2RP2000447	295	R-NT2RP2000447	1058
NT2RP2000479	F-NT2RP2000479	296	R-NT2RP2000479	1059
NT2RP2000514	F-NT2RP2000514	297	R-NT2RP2000514	1060
NT2RP2000533	F-NT2RP2000533	298	R-NT2RP2000533	1061
NT2RP2000610	F-NT2RP2000610	299		
NT2RP2000616	F-NT2RP2000616	300	R-NT2RP2000616	1062
NT2RP2000649	F-NT2RP2000649	301	R-NT2RP2000649	1063
NT2RP2000663	F-NT2RP2000663	302	R-NT2RP2000663	1064
NT2RP2000694	F-NT2RP2000694	303		
NT2RP2000712	F-NT2RP2000712	304	R-NT2RP2000712	1065
NT2RP2000739	F-NT2RP2000739	305	R-NT2RP2000739	1066
NT2RP2000818	F-NT2RP2000818	306	R-NT2RP2000818	1067
NT2RP2000903	F-NT2RP2000903	307	R-NT2RP2000903	1068
NT2RP2001200	F-NT2RP2001200	308	R-NT2RP2001200	1069
NT2RP2001223	F-NT2RP2001223	309	R-NT2RP2001223	1070
NT2RP2001276	F-NT2RP2001276	310	R-NT2RP2001276	1071
NT2RP2001388	F-NT2RP2001388	311	R-NT2RP2001388	1072
NT2RP2001469	F-NT2RP2001469	312	R-NT2RP2001469	1073
NT2RP2001480	F-NT2RP2001480	313	R-NT2RP2001480	1074
NT2RP2001495	F-NT2RP2001495	314	R-NT2RP2001495	1075
NT2RP2001514	F-NT2RP2001514	315	R-NT2RP2001514	1076
NT2RP2001529	F-NT2RP2001529	316		
NT2RP2001538	F-NT2RP2001538	317	R-NT2RP2001538	1077
NT2RP2001562	F-NT2RP2001562	318	R-NT2RP2001562	1078
NT2RP2001662	F-NT2RP2001662	319	R-NT2RP2001662	1079
NT2RP2001755	F-NT2RP2001755	320	R-NT2RP2001755	1080
NT2RP2001769	F-NT2RP2001769	321	R-NT2RP2001769	1081
NT2RP2001817	F-NT2RP2001817	322	R-NT2RP2001817	1082
NT2RP2001878	F-NT2RP2001878	323	R-NT2RP2001878	1083
NT2RP2001903	F-NT2RP2001903	324	R-NT2RP2001903	1084
NT2RP2001915	F-NT2RP2001915	325	R-NT2RP2001915	1085
NT2RP2001921	F-NT2RP2001921	326	R-NT2RP2001921	1086
NT2RP2001948	F-NT2RP2001948	327	R-NT2RP2001948	1087
NT2RP2001956	F-NT2RP2001956	328	R-NT2RP2001956	1088
NT2RP2002015	F-NT2RP2002015	329	R-NT2RP2002015	1089
NT2RP2002063	F-NT2RP2002063	330	R-NT2RP2002063	1090
NT2RP2002188	F-NT2RP2002188	331	R-NT2RP2002188	1091
NT2RP2002232	F-NT2RP2002232	332	R-NT2RP2002232	1092
NT2RP2002304	F-NT2RP2002304	333	R-nnnnnnnnnnnn	1093
NT2RP2002409	F-NT2RP2002409	334	R-NT2RP2002409	1094
NT2RP2002510	F-NT2RP2002510	335	R-NT2RP2002510	1095

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RP2002527	F-NT2RP2002527	336	R-NT2RP2002527	1096
NT2RP2002533	F-NT2RP2002533	337	R-NT2RP2002533	1097
NT2RP2002564	F-NT2RP2002564	338	R-NT2RP2002564	1098
NT2RP2002674	F-NT2RP2002674	339	R-NT2RP2002674	1099
NT2RP2002721	F-NT2RP2002721	340	R-NT2RP2002721	1100
NT2RP2002824	F-NT2RP2002824	341	R-NT2RP2002824	1101
NT2RP2002942	F-NT2RP2002942	342	R-NT2RP2002942	1102
NT2RP2002974	F-NT2RP2002974	343	R-NT2RP2002974	1103
NT2RP2002976	F-NT2RP2002976	344	R-NT2RP2002976	1104
NT2RP2003042	F-NT2RP2003042	345	R-NT2RP2003042	1105
NT2RP2003138	F-NT2RP2003138	346		
NT2RP2003179	F-NT2RP2003179	347	R-NT2RP2003179	1106
NT2RP2003210	F-NT2RP2003210	348	R-NT2RP2003210	1107
NT2RP2003302	F-NT2RP2003302	349	R-NT2RP2003302	1108
NT2RP2003369	F-NT2RP2003369	350	R-NT2RP2003369	1109
NT2RP2003383	F-NT2RP2003383	351	R-NT2RP2003383	1110
NT2RP2003390	F-NT2RP2003390	352	R-NT2RP2003390	1111
NT2RP2003469	F-NT2RP2003469	353	R-NT2RP2003469	1112
NT2RP2003545	F-NT2RP2003545	354	R-NT2RP2003545	1113
NT2RP2003593	F-NT2RP2003593	355	R-NT2RP2003593	1114
NT2RP2003599	F-NT2RP2003599	356	R-NT2RP2003599	1115
NT2RP2003655	F-NT2RP2003655	357	R-NT2RP2003655	1116
NT2RP2003664	F-NT2RP2003664	358	R-NT2RP2003664	1117
NT2RP2003931	F-NT2RP2003931	359	R-NT2RP2003931	1118
NT2RP2003940	F-NT2RP2003940	360	R-NT2RP2003940	1119
NT2RP2003950	F-NT2RP2003950	361	R-NT2RP2003950	1120
NT2RP2004069	F-NT2RP2004069	362	R-NT2RP2004069	1121
NT2RP2004108	F-NT2RP2004108	363	R-NT2RP2004108	1122
NT2RP2004141	F-NT2RP2004141	364	R-NT2RP2004141	1123
NT2RP2004179	F-NT2RP2004179	365	R-NT2RP2004179	1124
NT2RP2004205	F-NT2RP2004205	366	R-NT2RP2004205	1125
NT2RP2004447	F-NT2RP2004447	367	R-NT2RP2004447	1126
NT2RP2004495	F-NT2RP2004495	368	R-NT2RP2004495	1127
NT2RP2004524	F-NT2RP2004524	369	R-NT2RP2004524	1128
NT2RP2004556	F-NT2RP2004556	370	R-NT2RP2004556	1129
NT2RP2004606	F-NT2RP2004606	371	R-NT2RP2004606	1130
NT2RP2004648	F-NT2RP2004648	372	R-NT2RP2004648	1131
NT2RP2004670	F-NT2RP200467()	373	R-NT2RP2004670	1132
NT2RP2004794	F-NT2RP2004794	374	R-NT2RP2004794	1133
NT2RP2004837	F-NT2RP2004837	375	R-NT2RP2004837	1134
NT2RP2004847	F-NT2RP2004847	376	R-NT2RP2004847	1135
NT2RP2005027	F-NT2RP2005027	377	R-NT2RP2005027	1136
NT2RP2005069	F-NT2RP2005069	378	R-NT2RP2005069	1137
NT2RP2005163	F-NT2RP2005163	379	R-NT2RP2005163	1138
NT2RP2005181	F-NT2RP2005181	380	R-NT2RP2005181	1139
NT2RP2005247	F-NT2RP2005247	381	R-NT2RP2005247	1140
NT2RP2005378	F-NT2RP2005378	382	R-NT2RP2005378	1141
NT2RP2005391	F-NT2RP2005391	383	R-NT2RP2005391	1142

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RP2005425	F-NT2RP2005425	384	R-NT2RP2005425	1143
NT2RP2005463	F-NT2RP2005463	385	R-NT2RP2005463	1144
NT2RP2005514	F-NT2RP2005514	386	R-NT2RP2005514	1145
NT2RP2005535	F-NT2RP2005535	387	R-NT2RP2005535	1146
NT2RP2005541	F-NT2RP2005541	388	R-NT2RP2005541	1147
NT2RP2005597	F-NT2RP2005597	389	R-NT2RP2005597	1148
NT2RP2005632	F-NT2RP2005632	390	R-nnnnnnnnnnn	1149
NT2RP2005666	F-NT2RP2005666	391	R-NT2RP2005666	1150
NT2RP2005774	F-NT2RP2005774	392	R-NT2RP2005774	1151
NT2RP2005878	F-NT2RP2005878	393	R-NT2RP2005878	1152
NT2RP2005883	F-NT2RP2005883	394	R-NT2RP2005883	1153
NT2RP2005887	F-NT2RP2005887	395	R-NT2RP2005887	1154
NT2RP2005941	F-NT2RP2005941	396	R-nnnnnnnnnnn	1155
NT2RP2005994	F-NT2RP2005994	397	R-NT2RP2005994	1156
NT2RP2006004	F-NT2RP2006004	398	R-NT2RP2006004	1157
NT2RP2006042	F-NT2RP2006042	399	R-NT2RP2006042	1158
NT2RP2006092	F-NT2RP2006092	400	R-NT2RP2006092	1159
NT2RP2006099	F-NT2RP2006099	401	R-NT2RP2006099	1160
NT2RP2006134	F-NT2RP2006134	402	R-NT2RP2006134	1161
NT2RP2006269	F-NT2RP2006269	403	R-NT2RP2006269	1162
NT2RP2006512	F-NT2RP2006512	404	R-NT2RP2006512	1163
NT2RP3000011	F-NT2RP3000011	405	R-NT2RP3000011	1164
NT2RP3000022	F-NT2RP3000022	406	R-NT2RP3000022	1165
NT2RP3000059	F-NT2RP3000059	407	R-NT2RP3000059	1166
NT2RP3000063	F-NT2RP3000063	408	R-NT2RP3000063	1167
NT2RP3000125	F-NT2RP3000125	409	R-nnnnnnnnnnn	1168
NT2RP3000148	F-NT2RP3000148	410	R-NT2RP3000148	1169
NT2RP3000169	F-NT2RP3000169	411	R-NT2RP3000169	1170
NT2RP3000171	F-NT2RP3000171	412	R-NT2RP3000171	1171
NT2RP3000172	F-NT2RP3000172	413	R-NT2RP3000172	1172
NT2RP3000201	F-NT2RP3000201	414	R-NT2RP3000201	1173
NT2RP3000232	F-NT2RP3000232	415	R-NT2RP3000232	1174
NT2RP3000304	F-NT2RP3000304	416	R-NT2RP3000304	1175
NT2RP3000378	F-NT2RP3000378	417	R-NT2RP3000378	1176
NT2RP3000427	F-NT2RP3000427	418		
NT2RP3000436	F-NT2RP3000436	419	R-NT2RP3000436	1177
NT2RP3000444	F-NT2RP3000444	420	R-NT2RP3000444	1178
NT2RP3000460	F-NT2RP3000460	421	R-NT2RP3000460	1179
NT2RP3000481	F-NT2RP3000481	422	R-NT2RP3000481	1180
NT2RP3000616	F-NT2RP3000616	423	R-NT2RP3000616	1181
NT2RP3000645	F-NT2RP3000645	424	R-NT2RP3000645	1182
NT2RP3000652	F-NT2RP3000652	425	R-NT2RP3000652	1183
NT2RP3000676	F-NT2RP3000676	426	R-NT2RP3000676	1184
NT2RP3000677	F-NT2RP3000677	427	R-NT2RP3000677	1185
NT2RP3000721	F-NT2RP3000721	428	R-NT2RP3000721	1186
NT2RP3000789	F-NT2RP3000789	429	R-NT2RP3000789	1187
NT2RP3000818	F-NT2RP3000818	430	R-NT2RP3000818	1188
NT2RP3000820	F-NT2RP3000820	431	R-NT2RP3000820	1189

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RP3000838	F-NT2RP3000838	432	R-NT2RP3000838	1190
NT2RP3000871	F-NT2RP3000871	433	R-NT2RP3000871	1191
NT2RP3000907	F-NT2RP3000907	434	R-NT2RP3000907	1192
NT2RP3000921	F-NT2RP3000921	435	R-NT2RP3000921	1193
NT2RP3001012	F-NT2RP3001012	436	R-NT2RP3001012	1194
NT2RP3001044	F-NT2RP3001044	437	R-NT2RP3001044	1195
NT2RP3001061	F-NT2RP3001061	438	R-NT2RP3001061	1196
NT2RP3001159	F-NT2RP3001159	439	R-NT2RP3001159	1197
NT2RP3001170	F-NT2RP3001170	440	R-NT2RP3001170	1198
NT2RP3001195	F-NT2RP3001195	441	R-NT2RP3001195	1199
NT2RP3001240	F-NT2RP3001240	442	R-NT2RP3001240	1200
NT2RP3001271	F-NT2RP3001271	443	R-NT2RP3001271	1201
NT2RP3001322	F-NT2RP3001322	444	R-NT2RP3001322	1202
NT2RP3001388	F-NT2RP3001388	445		
NT2RP3001542	F-NT2RP3001542	446	R-NT2RP3001542	1203
NT2RP3001560	F-NT2RP3001560	447	R-NT2RP3001560	1204
NT2RP3001592	F-NT2RP3001592	448	R-NT2RP3001592	1205
NT2RP3001650	F-NT2RP3001650	449		
NT2RP3001685	F-NT2RP3001685	450	R-NT2RP3001685	1206
NT2RP3001738	F-NT2RP3001738	451	R-NT2RP3001738	1207
NT2RP3001754	F-NT2RP3001754	452	R-NT2RP3001754	1208
NT2RP3001858	F-NT2RP3001858	453	R-NT2RP3001858	1209
NT2RP3001976	F-NT2RP3001976	454	R-NT2RP3001976	1210
NT2RP3002015	F-NT2RP3002015	455	R-NT2RP3002015	1211
NT2RP3002160	F-NT2RP3002160	456	R-NT2RP3002160	1212
NT2RP3002281	F-NT2RP3002281	457	R-NT2RP3002281	1213
NT2RP3002286	F-NT2RP3002286	458	R-NT2RP3002286	1214
NT2RP3002311	F-NT2RP3002311	459	R-NT2RP3002311	1215
NT2RP3002324	F-NT2RP3002324	460	R-NT2RP3002324	1216
NT2RP3002342	F-NT2RP3002342	461	R-NT2RP3002342	1217
NT2RP3002353	F-NT2RP3002353	462	R-NT2RP3002353	1218
NT2RP3002409	F-NT2RP3002409	463	R-NT2RP3002409	1219
NT2RP3002411	F-NT2RP3002411	464	R-NT2RP3002411	1220
NT2RP3002448	F-NT2RP3002448	465	R-NT2RP3002448	1221
NT2RP3002571	F-NT2RP3002571	466	R-NT2RP3002571	1222
NT2RP3002664	F-NT2RP3002664	467	R-NT2RP3002664	1223
NT2RP3002721	F-NT2RP3002721	468	R-NT2RP3002721	1224
NT2RP3002737	F-NT2RP3002737	469	R-NT2RP3002737	1225
NT2RP3002738	F-NT2RP3002738	470	R-NT2RP3002738	1226
NT2RP3002790	F-NT2RP3002790	471	R-NT2RP3002790	1227
NT2RP3002836	F-NT2RP3002836	472	R-NT2RP3002836	1228
NT2RP3002887	F-NT2RP3002887	473	R-NT2RP3002887	1229
NT2RP3002900	F-NT2RP3002900	474	R-NT2RP3002900	1230
NT2RP3002958	F-NT2RP3002958	475	R-NT2RP3002958	1231
NT2RP3002983	F-NT2RP3002983	476	R-NT2RP3002983	1232
NT2RP3003000	F-NT2RP3003000	477	R-NT2RP3003000	1233
NT2RP3003076	F-NT2RP3003076	478	R-NT2RP3003076	1234
NT2RP3003354	F-NT2RP3003354	479	R-NT2RP3003354	1235

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
NT2RP3003448	F-NT2RP3003448	480	R-NT2RP3003448	1236
NT2RP3003469	F-NT2RP3003469	481	R-NT2RP3003469	1237
NT2RP3003473	F-NT2RP3003473	482	R-NT2RP3003473	1238
NT2RP3003527	F-NT2RP3003527	483	R-NT2RP3003527	1239
NT2RP3003532	F-NT2RP3003532	484	R-NT2RP3003532	1240
NT2RP3003535	F-NT2RP3003535	485	R-nnnnnnnnnnn	1241
NT2RP3003559	F-NT2RP3003559	486	R-NT2RP3003559	1242
NT2RP3003614	F-NT2RP3003614	487	R-NT2RP3003614	1243
NT2RP3003729	F-NT2RP3003729	488	R-NT2RP3003729	1244
NT2RP3003849	F-NT2RP3003849	489	R-NT2RP3003849	1245
NT2RP3003874	F-NT2RP3003874	490	R-NT2RP3003874	1246
NT2RP3003939	F-NT2RP3003939	491		
NT2RP3003963	F-NT2RP3003963	492	R-NT2RP3003963	1247
NT2RP3004000	F-NT2RP3004000	493	R-NT2RP3004000	1248
NT2RP3004025	F-NT2RP3004025	494	R-NT2RP3004025	1249
NT2RP3004067	F-NT2RP3004067	495		
NT2RP3004075	F-NT2RP3004075	496	R-NT2RP3004075	1250
NT2RP3004083	F-NT2RP3004083	497	R-NT2RP3004083	1251
NT2RP3004090	F-NT2RP3004090	498	R-NT2RP3004090	1252
NT2RP3004119	F-NT2RP3004119	499	R-NT2RP3004119	1253
NT2RP3004130	F-NT2RP3004130	500	R-NT2RP3004130	1254
NT2RP3004133	F-NT2RP3004133	501	R-NT2RP3004133	1255
NT2RP3004202	F-NT2RP3004202	502	R-NT2RP3004202	1256
NT2RP3004294	F-NT2RP3004294	503	R-NT2RP3004294	1257
NT2RP3004309	F-NT2RP3004309	504	R-NT2RP3004309	1258
NT2RP3004321	F-NT2RP3004321	505	R-NT2RP3004321	1259
NT2RP3004345	F-NT2RP3004345	506	R-NT2RP3004345	1260
NT2RP3004355	F-NT2RP3004355	507	R-NT2RP3004355	1261
NT2RP3004374	F-NT2RP3004374	508	R-NT2RP3004374	1262
NT2RP3004406	F-NT2RP3004406	509	R-NT2RP3004406	1263
NT2RP3004481	F-NT2RP3004481	510	R-NT2RP3004481	1264
NT2RP3004552	F-NT2RP3004552	511	R-NT2RP3004552	1265
NT2RP3004557	F-NT2RP3004557	512		
NT2RP3004625	F-NT2RP3004625	513	R-NT2RP3004625	1266
NT2RP3004640	F-NT2RP3004640	514	R-NT2RP3004640	1267
NT2RP3004647	F-NT2RP3004647	515	R-NT2RP3004647	1268
NT2RP4000108	F-NT2RP4000108	516	R-NT2RP4000108	1269
NT2RP4000634	F-NT2RP4000634	517	R-NT2RP4000634	1270
NT2RP4000962	F-NT2RP4000962	518	R-NT2RP4000962	1271
NT2RP4001001	F-NT2RP4001001	519	R-NT2RP4001001	1272
NT2RP4001009	F-NT2RP4001009	520	R-NT2RP4001009	1273
NT2RP4001467	F-NT2RP4001467	521	R-NT2RP4001467	1274
NT2RP4001877	F-NT2RP4001877	522	R-NT2RP4001877	1275
NT2RP4001879	F-NT2RP4001879	523	R-NT2RP4001879	1276
NT2RP4002187	F-NT2RP4002187	524	R-NT2RP4002187	1277
NT2RP4002451	F-NT2RP4002451	525	R-NT2RP4002451	1278
NT2RP4002715	F-NT2RP4002715	526	R-NT2RP4002715	1279
NT2RP4002750	F-NT2RP4002750	527	R-NT2RP4002750	1280

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
OVARC1000003	F-OVARC1000003	528	R-OVARC1000003	1281
OVARC1000090	F-OVARC1000090	529	R-OVARC1000090	1282
OVARC1000105	F-OVARC1000105	530	R-OVARC1000105	1283
OVARC1000137	F-OVARC1000137	531	R-OVARC1000137	1284
OVARC1000208	F-OVARC1000208	532	R-OVARC1000208	1285
OVARC1000255	F-OVARC1000255	533	R-OVARC1000255	1286
OVARC1000275	F-OVARC1000275	534	R-OVARC1000275	1287
OVARC1000298	F-OVARC1000298	535	R-OVARC1000298	1288
OVARC1000307	F-OVARC1000307	536	R-OVARC1000307	1289
OVARC1000313	F-OVARC1000313	537	R-OVARC1000313	1290
OVARC1000331	F-OVARC1000331	538	R-OVARC1000331	1291
OVARC1000410	F-OVARC1000410	539	R-OVARC1000410	1292
OVARC1000439	F-OVARC1000439	540	R-OVARC1000439	1293
OVARC1000467	F-OVARC1000467	541	R-OVARC1000467	1294
OVARC1000529	F-OVARC1000529	542	R-OVARC1000529	1295
OVARC1000553	F-OVARC1000553	543	R-OVARC1000553	1296
OVARC1000775	F-OVARC1000775	544	R-OVARC1000775	1297
OVARC1000811	F-OVARC1000811	545	R-OVARC1000811	1298
OVARC1000853	F-OVARC1000853	546	R-OVARC1000853	1299
OVARC1000873	F-OVARC1000873	547	R-OVARC1000873	1300
OVARC1000916	F-OVARC1000916	548	R-OVARC1000916	1301
OVARC1000956	F-OVARC1000956	549	R-OVARC1000956	1302
OVARC1000995	F-OVARC1000995	550	R-OVARC1000995	1303
OVARC1001030	F-OVARC1001030	551	R-OVARC1001030	1304
OVARC1001049	F-OVARC1001049	552	R-OVARC1001049	1305
OVARC1001086	F-OVARC1001086	553	R-OVARC1001086	1306
OVARC1001132	F-OVARC1001132	554	R-OVARC1001132	1307
OVARC1001163	F-OVARC1001163	555	R-OVARC1001163	1308
OVARC1001222	F-OVARC1001222	556	R-OVARC1001222	1309
OVARC1001260	F-OVARC1001260	557	R-OVARC1001260	1310
OVARC1001336	F-OVARC1001336	558	R-OVARC1001336	1311
OVARC1001338	F-OVARC1001338	559	R-OVARC1001338	1312
OVARC1001569	F-OVARC1001569	560	R-OVARC1001569	1313
OVARC1001570	F-OVARC1001570	561	R-OVARC1001570	1314
OVARC1001596	F-OVARC1001596	562	R-OVARC1001596	1315
OVARC1001607	F-OVARC1001607	563	R-OVARC1001607	1316
OVARC1001725	F-OVARC1001725	564	R-OVARC1001725	1317
OVARC1001727	F-OVARC1001727	565	R-OVARC1001727	1318
OVARC1001807	F-OVARC1001807	566	R-OVARC1001807	1319
OVARC1001833	F-OVARC1001833	567	R-OVARC1001833	1320
OVARC1001952	F-OVARC1001952	568		
OVARC1001991	F-OVARC1001991	569	R-OVARC1001991	1321
OVARC1002058	F-OVARC1002058	570	R-OVARC1002058	1322
OVARC1002178	F-OVARC1002178	571	R-OVARC1002178	1323
PLACE 1000033	F-PLACE1000033	572	R-PLACE1000033	1324
PLACE 1000231	F-PLACE1000231	573	R-PLACE1000231	1325
PLACE 1000258	F-PLACE1000258	574	R-PLACE1000258	1326
PLACE 1000442	F-PLACE1000442	575	R-PLACE1000442	1327

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
PLACE 1000560	F-PLACE1000560	576	R-PLACE1000560	1328
PLACE 1000740	F-PLACE1000740	577	R-PLACE1000740	1329
PLACE 1000907	F-PLACE1000907	578		
PLACE 1000912	F-PLACE1000912	579	R-PLACE1000912	1330
PLACE 1000914	F-PLACE1000914	580	R-PLACE1000914	1331
PLACE 1000927	F-PLACE1000927	581	R-PLACE1000927	1332
PLACE 1000986	F-PLACE1000986	582	R-PLACE1000986	1333
PLACE1001016	F-PLACE1001016	583	R-PLACE1001016	1334
PLACE 1001100	F-PLACE1001100	584	R-PLACE1001100	1335
PLACE 1001114	F-PLACE1001114	585	R-PLACE1001114	1336
PLACE 1001123	F-PLACE1001123	586	R-PLACE1001123	1337
PLACE 1001183	F-PLACE1001183	587	R-PLACE1001183	1338
PLACE 1001229	F-PLACE1001229	588	R-PLACE1001229	1339
PLACE 1001231	F-PLACE1001231	589	R-PLACE1001231	1340
PLACE 1001340	F-PLACE1001340	590	R-PLACE1001340	1341
PLACE1001401	F-PLACE1001401	591	R-PLACE1001401	1342
PLACE 1001407	F-PLACE1001407	592	R-PLACE1001407	1343
PLACE 1001464	F-PLACE1001464	593	R-PLACE1001464	1344
PLACE1001500	F-PLACE1001500	594	R-PLACE1001500	1345
PLACE1001516	F-PLACE1001516	595	R-PLACE1001516	1346
PLACE1001536	F-PLACE1001536	596	R-PLACE1001536	1347
PLACE 1001564	F-PLACE1001564	597	R-PLACE1001564	1348
PLACE 1001655	F-PLACE1001655	598	R-PLACE1001655	1349
PLACE 1001788	F-PLACE1001788	599	R-PLACE1001788	1350
PLACE1001795	F-PLACE1001795	600	R-PLACE1001795	1351
PLACE1001836	F-PLACE1001836	601	R-PLACE1001836	1352
PLACE 1001918	F-PLACE1001918	602	R-PLACE1001918	1353
PLACE 1001949	F-PLACE1001949	603	R-PLACE1001949	1354
PLACE 1002080	F-PLACE1002080	604	R-PLACE1002080	1355
PLACE 1002095	F-PLACE1002095	605	R-PLACE1002095	1356
PLACE 1002153	F-PLACE1002153	606	R-PLACE1002153	1357
PLACE 1002329	F-PLACE1002329	607	R-PLACE1002329	1358
PLACE 1002355	F-PLACE1002355	608	R-PLACE1002355	1359
PLACE1002374	F-PLACE1002374	609	R-PLACE1002374	1360
PLACE 1002518	F-PLACE1002518	610	R-PLACE1002518	1361
PLACE 1002547	F-PLACE1002547	611	R-PLACE1002547	1362
PLACE 1002726	F-PLACE1002726	612	R-PLACE1002726	1363
PLACE 1002905	F-PLACE1002905	613	R-PLACE1002905	1364
PLACE 1002911	F-PLACE1002911	614	R-PLACE1002911	1365
PLACE 1002967	F-PLACE1002967	615	R-PLACE1002967	1366
PLACE 1003135	F-PLACE1003135	616	R-PLACE1003135	1367
PLACE1003163	F-PLACE1003163	617	R-PLACE1003163	1368
PLACE 1003407	F-PLACE1003407	618	R-PLACE1003407	1369
PLACE 1003428	F-PLACE1003428	619	R-PLACE1003428	1370
PLACE1003438	F-PLACE1003438	620	R-PLACE1003438	1371
PLACE 1003460	F-PLACE1003460	621	R-PLACE1003460	1372
PLACE 1003529	F-PLACE1003529	622	R-nnnnnnnnnnn	1373
PLACE 1003573	F-PLACE1003573	623	R-PLACE1003573	1374

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
PLACE 1003598	F-PLACE1003598	624	R-PLACE1003598	1375
PLACE1003644	F-PLACE1003644	625	R-PLACE1003644	1376
PLACE1003737	F-PLACE1003737	626	R-PLACE1003737	1377
PLACE 1003772	F-PLACE1003772	627	R-PLACE1003772	1378
PLACE 1003839	F-PLACE1003839	628	R-PLACE1003839	1379
PLACE 1003845	F-PLACE1003845	629	R-PLACE1003845	1380
PLACE 1003 852	F-PLACE1003852	630	R-PLACE1003852	1381
PLACE 1004028	F-PLACE1004028	631	R-PLACE1004028	1382
PLACE 1004078	F-PLACE1004078	632	R-PLACE1004078	1383
PLACE1004166	F-PLACE1004166	633	R-PLACE1004166	1384
PLACE 1004168	F-PLACE1004168	634	R-nnnnnnnnnnnn	1385
PLACE1004199	F-PLACE1004199	635	R-PLACE1004199	1386
PLACE 1004279	F-PLACE1004279	636	R-PLACE1004279	1387
PLACE 1004282	F-PLACE1004282	637	R-PLACE1004282	1388
PLACE 1004305	F-PLACE1004305	638	R-PLACE1004305	1389
PLACE 1004441	F-PLACE1004441	639	R-PLACE1004441	1390
PLACE 1004450	F-PLACE1004450	640	R-PLACE1004450	1391
PLACE 1004482	F-PLACE1004482	641	R-PLACE1004482	1392
PLACE 1004492	F-PLACE1004492	642	R-PLACE1004492	1393
PLACE 1004519	F-PLACE1004519	643	R-PLACE1004519	1394
PLACE 1004520	F-PLACE1004520	644	R-PLACE1004520	1395
PLACE 1004630	F-PLACE1004630	645	R-PLACE1004630	1396
PLACE 1004637	F-PLACE1004637	646	R-PLACE1004637	1397
PLACE 1004648	F-PLACE1004648	647	R-PLACE1004648	1398
PLACE 1004816	F-PLACE1004816	648	R-PLACE1004816	1399
PLACE 1004887	F-PLACE1004887	649	R-PLACE1004887	1400
PLACE 1005003	F-PLACE1005003	650	R-PLACE1005003	1401
PLACE 1005005	F-PLACE1005005	651	R-PLACE1005005	1402
PLACE 1005031	F-PLACE1005031	652	R-PLACE1005031	1403
PLACE 1005239	F-PLACE1005239	653	R-PLACE1005239	1404
PLACE 1005250	F-PLACE1005250	654	R-PLACE1005250	1405
PLACE 1005383	F-PLACE1005383	655	R-PLACE1005383	1406
PLACE 1005410	F-PLACE1005410	656	R-PLACE1005410	1407
PLACE 1005426	F-PLACE1005426	657	R-PLACE1005426	1408
PLACE 1005519	F-PLACE1005519	658	R-PLACE1005519	1409
PLACE 1005539	F-PLACE1005539	659	R-PLACE1005539	1410
PLACE 1005544	F-PLACE1005544	660	R-PLACE1005544	1411
PLACE 1005569	F-PLACE1005569	661	R-PLACE1005569	1412
PLACE 1005601	F-PLACE1005601	662	R-PLACE1005601	1413
PLACE 1005660	F-PLACE1005660	663	R-PLACE1005660	1414
PLACE 1005669	F-PLACE1005669	664	R-PLACE1005669	1415
PLACE 1005682	F-PLACE1005682	665	R-PLACE1005682	1416
PLACE 1005725	F-PLACE1005725	666	R-PLACE1005725	1417
PLACE 1005736	F-PLACE1005736	667	R-PLACE1005736	1418
PLACE 1005745	F-PLACE1005745	668	R-PLACE1005745	1419
PLACE 1005768	F-PLACE1005768	669	R-PLACE1005768	1420
PLACE1005815	F-PLACE1005815	670	R-PLACE1005815	1421
PLACE 1005878	F-PLACE1005878	671	R-PLACE1005878	1422

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
PLACE 1005927	F-PLACE1005927	672	R-PLACE1005927	1423
PLACE 1006071	F-PLACE1006071	673	R-PLACE1006071	1424
PLACE 1006073	F-PLACE1006073	674	R-PLACE1006073	1425
PLACE 1006079	F-PLACE1006079	675	R-PLACE1006079	1426
PLACE 1006093	F-PLACE1006093	676	R-PLACE1006093	1427
PLACE 1006208	F-PLACE1006208	677	R-nnnnnnnnnnn	1428
PLACE 1006219	F-PLACE1006219	678	R-PLACE1006219	1429
PLACE 1006277	F-PLACE1006277	679	R-PLACE1006277	1430
PLACE 1006290	F-PLACE1006290	680	R-PLACE1006290	1431
PLACE 1006443	F-PLACE1006443	681	R-PLACE1006443	1432
PLACE 1006515	F-PLACE1006515	682	R-PLACE1006515	1433
PLACE 1006716	F-PLACE1006716	683	R-PLACE1006716	1434
PLACE 1006786	F-PLACE1006786	684	R-PLACE1006786	1435
PLACE 1006809	F-PLACE1006809	685	R-PLACE1006809	1436
PLACE 1006959	F-PLACE1006959	686	R-PLACE1006959	1437
PLACE 1007028	F-PLACE1007028	687	R-PLACE1007028	1438
PLACE 1007040	F-PLACE1007040	688	R-PLACE1007040	1439
PLACE 1007077	F-PLACE1007077	689	R-PLACE1007077	1440
PLACE 1007081	F-PLACE1007081	690	R-PLACE1007081	1441
PLACE 1007096	F-PLACE1007096	691	R-PLACE1007096	1442
PLACE 1007296	F-PLACE1007296	692	R-PLACE1007296	1443
PLACE 1007591	F-PLACE1007591	693	R-PLACE1007591	1444
PLACE1007626	F-PLACE1007626	694	R-PLACE1007626	1445
PLACE 1007702	F-PLACE1007702	695	R-PLACE1007702	1446
PLACE1007845	F-PLACE1007845	696	R-PLACE1007845	1447
PLACE1007881	F-PLACE1007881	697	R-PLACE1007881	1448
PLACE 1007971	F-PLACE1007971	698	R-PLACE1007971	1449
PLACE 1008282	F-PLACE1008282	699	R-PLACE1008282	1450
PLACE 1008297	F-PLACE1008297	700	R-PLACE1008297	1451
PLACE 1008359	F-PLACE1008359	701	R-PLACE1008359	1452
PLACE 1008469	F-PLACE1008469	702	R-PLACE1008469	1453
PLACE 1008549	F-PLACE1008549	703	R-PLACE1008549	1454
PLACE 1008657	F-PLACE1008657	704	R-PLACE1008657	1455
PLACE 1008716	F-PLACE1008716	705	R-PLACE1008716	1456
PLACE 1008744	F-PLACE1008744	706	R-PLACE1008744	1457
PLACE 1008984	F-PLACE1008984	707	R-PLACE1008984	1458
PLACE 1008985	F-PLACE1008985	708	R-PLACE1008985	1459
PLACE 1009067	F-PLACE1009067	709	R-PLACE1009067	1460
PLACE 1009196	F-PLACE1009196	710	R-PLACE1009196	1461
PLACE 1009279	F-PLACE1009279	711	R-PLACE1009279	1462
PLACE 1009527	F-PLACE1009527	712	R-PLACE1009527	1463
PLACE 1009546	F-PLACE1009546	713	R-PLACE1009546	1464
PLACE 1009600	F-PLACE1009600	714	R-PLACE1009600	1465
PLACE 1009735	F-PLACE1009735	715	R-PLACE1009735	1466
PLACE 1009982	F-PLACE1009982	716	R-nnnnnnnnnnn	1467
PLACE1010011	F-PLACE1010011	717	R-PLACE1010011	1468
PLACE1010078	F-PLACE1010078	718	R-PLACE1010078	1469
PLACE1010081	F-PLACE1010081	719	R-PLACE1010081	1470

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
PLACE 1010251	F-PLACE1010251	720	R-PLACE1010251	1471
PLACE1010445	F-PLACE1010445	721	R-PLACE1010445	1472
PLACE 1010713	F-PLACE1010713	722	R-PLACE1010713	1473
PLACE 1010784	F-PLACE1010784	723	R-PLACE1010784	1474
PLACE 1010827	F-PLACE1010827	724	R-PLACE1010827	1475
PLACE 1010968	F-PLACE1010968	725	R-PLACE1010968	1476
PLACE 1011045	F-PLACE1011045	726	R-PLACE1011045	1477
PLACE1011116	F-PLACE1011116	727	R-PLACE1011116	1478
PLACE1011181	F-PLACE1011181	728		
PLACE1011236	F-PLACE1011236	729	R-PLACE1011236	1479
PLACE 1011364	F-PLACE1011364	730	R-PLACE1011364	1480
PLACE 1 011407	F-PLACE1011407	731	R-PLACE1011407	1481
PLACE1011516	F-PLACE1011516	732	R-PLACE1011516	1482
PLACE 1011708	F-PLACE1011708	733	R-PLACE1011708	1483
PLACE 1011824	F-PLACE1011824	734	R-PLACE1011824	1484
PLACE 1011978	F-PLACE1011978	735	R-PLACE1011978	1485
PLACE2000118	F-PLACE2000118	736	R-PLACE2000118	1486
PLACE2000219	F-PLACE2000219	737	R-PLACE2000219	1487
PLACE3000181	F-PLACE3000181	738	R-PLACE3000181	1488
PLACE3000213	F-PLACE3000213	739	R-PLACE3000213	1489
PLACE4000354	F-PLACE4000354	740	R-PLACE4000354	1490
PLACE4000455	F-PLACE4000455	741	R-PLACE4000455	1491
SKNMC1000004	F-SKNMC1000004	742		
SKNMC1000014	F-SKNMC1000014	743		
SKNMC1000082	F-SKNMC1000082	744		
THYRO1000036	F-THYRO1000036	745	R-THYRO1000036	1492
THYRO1000061	F-THYRO1000061	746	R-THYRO1000061	1493
THYRO1000099	F-THYRO1000099	747	R-THYRO1000099	1494
THYRO1000196	F-THYRO1000196	748	R-THYRO1000196	1495
THYRO1000400	F-THYRO1000400	749	R-THYRO1000400	1496
THYRO1000580	F-THYRO1000580	750	R-THYRO1000580	1497
THYRO1000584	F-THYRO1000584	751	R-THYRO1000584	1498
THYRO1000678	F-THYRO1000678	752	R-THYRO1000678	1499
THYRO1000776	F-THYRO1000776	753	R-THYRO1000776	1500
THYRO1000795	F-THYRO1000795	754	R-THYRO1000795	1501
THYRO1000846	F-THYRO1000846	755	R-THYRO1000846	1502
THYRO1000866	F-THYRO1000866	756	R-THYRO1000866	1503
THYRO1000956	F-THYRO1000956	757	R-THYRO1000956	1504
THYRO1000964	F-THYRO1000964	758	R-THYRO1000964	1505
THYRO1000999	F-THYRO1000999	759	R-THYRO1000999	1506
THYRO1001063	F-THYRO1001063	760	R-THYRO1001063	1507
THYRO1001071	F-THYRO1001071	761	R-THYRO1001071	1508
THYR01001102	F-THYRO1001102	762	R-THYRO1001102	1509
THYRO1001113	F-THYRO1001113	763	R-THYRO1001113	1510
THYRO1001128	F-THYRO1001128	764	R-THYRO1001128	1511
THYRO1001205	F-THYRO1001205	765	R-THYRO1001205	1512
THYRO1001237	F-THYRO1001237	766	R-THYRO1001237	1513
THYRO1001242	F-THYRO1001242	767	R-THYRO1001242	1514

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
THYRO1001266	F-THYRO1001266	768	R-THYRO1001266	1515
THYRO1001327	F-THYRO1001327	769	R-THYRO1001327	1516
THYRO1001456	F-THYRO1001456	770	R-THYRO1001456	1517
THYRO1001457	F-THYRO1001457	771	R-THYRO1001457	1518
THYRO1001471	F-THYRO1001471	772	R-THYRO1001471	1519
THYRO1001478	F-THYRO1001478	773	R-THYRO1001478	1520
THYRO1001495	F-THYRO1001495	774	R-THYRO1001495	1521
THYRO1001523	F-THYRO1001523	775	R-THYRO1001523	1522
THYRO1001529	F-THYRO1001529	776	R-THYRO1001529	1523
THYRO1001593	F-THYRO1001593	777	R-THYRO1001593	1524
THYRO1001608	F-THYRO1001608	778	R-THYRO1001608	1525
THYRO1001641	F-THYRO1001641	779	R-THYRO1001641	1526
THYRO1001700	F-THYRO1001700	780	R-THYRO1001700	1527
THYRO1001702	F-THYRO1001702	781	R-THYRO1001702	1528
THYRO1001725	F-THYRO1001725	782	R-THYRO1001725	1529
THYRO1001770	F-THYRO1001770	783	R-THYRO1001770	1530
THYRO1001803	F-THYRO1001803	784	R-THYRO1001803	1531
Y79AA1000030	F-Y79AA1000030	785	R-Y79AA1000030	1532
Y79AA1000127	F-Y79AA1000127	786	R-Y79AA1000127	1533
Y79AA1000207	F-Y79AA1000207	787	R-Y79AA1000207	1534
Y79AA1000226	F-Y79AA1000226	788	R-Y79AA1000226	1535
Y79AA1000270	F-Y79AA1000270	789	R-Y79AA1000270	1536
Y79AA1000426	F-Y79AA1000426	790	R-Y79AA1000426	1537
Y79AA1000521	F-Y79AA1000521	791	R-Y79AA1000521	1538
Y79AA1000750	F-Y79AA1000750	792	R-Y79AA1000750	1539
Y79AA1000776	F-Y79AA1000776	793	R-Y79AA1000776	1540
Y79AA1000777	F-Y79AA1000777	794	R-Y79AA1000777	1541
Y79AA1000876	F-Y79AA1000876	795	R-Y79AA1000876	1542
Y79AA1000888	F-Y79AA1000888	796		
Y79AA1000959	F-Y79AA1000959	797	R-Y79AA1000959	1543
Y79AA1000967	F-Y79AA1000967	798	R-Y79AA1000967	1544
Y79AA1001013	F-Y79AA1001013	799	R-Y79AA1001013	1545
Y79AA1001056	F-Y79AA1001056	800	R-Y79AA1001056	1546
Y79AA1001062	F-Y79AA1001062	801	R-Y79AA1001062	1547
Y79AA1001090	F-Y79AA1001090	802	R-Y79AA1001090	1548
Y79AA1001212	F-Y79AA1001212	803	R-Y79AA1001212	1549
Y79AA1001264	F-Y79AA1001264	804	R-Y79AA1001264	1550
Y79AA1001272	F-Y79AA1001272	805	R-Y79AA1001272	1551
Y79AA1001328	F-Y79AA1001328	806	R-Y79AA1001328	1552
Y79AA1001426	F-Y79AA1001426	807	R-Y79AA1001426	1553
Y79AA1001427	F-Y79AA1001427	808		
Y79AA1001430	F-Y79AA1001430	809	R-Y79AA1001430	1554
Y79AA1001523	F-Y79AA1001523	810	R-Y79AA1001523	1555
Y79AA1001530	F-Y79AA1001530	811	R-Y79AA1001530	1556
Y79AA1001592	F-Y79AA1001592	812	R-Y79AA1001592	1557
Y79AA1001727	F-Y79AA1001727	813	R-Y79AA1001727	1558
Y79AA1001787	F-Y79AA1001787	814	R-Y79AA1001787	1559
Y79AA1001793	F-Y79AA1001793	815		

Table 1 (continued)

Correspondence between names of clone and the sequence name, and the SEQ ID.				
Name of clone	Name of 5'-sequence	SEQ ID	3 Name of 3'-sequence	SEQ ID
Y79AA1001795	F-Y79AA1001795	816	R-Y79AA1001795	1560
Y79AA1001799	F-Y79AA1001799	817	R-Y79AA1001799	1561
Y79AA1001803	F-Y79AA1001803	818	R-Y79AA1001803	1562
Y79AA1001863	F-Y79AA1001863	819	R-Y79AA1001863	1563
Y79AA1002022	F-Y79AA1002022	820	R-Y79AA1002022	1564
Y79AA1002058	F-Y79AA1002058	821		
Y79AA1002121	F-Y79AA1002121	822	R-nnnnnnnnnnnn	1565
Y79AA1002129	F-Y79AA1002129	823	R-nnnnnnnnnnnn	1566
Y79AA1002213	F-Y79AA1002213	824	R-Y79AA1002213	1567
Y79AA1002334	F-Y79AA1002334	825	R-Y79AA1002334	1568
Y79AA1002373	F-Y79AA1002373	826	R-Y79AA1002373	1569
Y79AA1002376	F-Y79AA1002376	827	R-Y79AA1002376	1570
Y79AA1002378	F-Y79AA1002378	828	R-Y79AA1002378	1571
Y79AA1002381	F-Y79AA1002381	829	R-Y79AA1002381	1572
NT2RP2006580	F-NT2RP2006580	2545	R-NT2RP2006580	2546

The sequence name starting from "F" means the name of 5'-end sequence, and the sequence name starting from "R" means the name of 3'-end sequence. A blank indicates that the 3'-end sequence corresponding to the 5'-end sequence has not been determined in the clone.

[0018] Furthermore, the present invention relates to the use of the above primers, as described below.

(4) A polynucleotide which can be synthesized with the primer set of (2) or (3).
(5) A polynucleotide comprising a coding region in the polynucleotide of (4).
(6) A substantially pure protein encoded by polynucleotide of (4).
(7) A partial peptide of the protein of (6).

[0019] In addition, the present invention comprises a polynucleotide described below and a protein encoded by the polynucleotide.

(8) An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the SEQ ID NOs in Table 370;
(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence set forth in any one of the SEQ ID NOs in Table 370;
(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences set forth in the SEQ ID NOs in Table 370, in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences set forth in the SEQ ID NOs in Table 370;
(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Table 370, and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Table 370;
(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);
(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence set forth in any one of the SEQ ID NOs in Table 370.

(9). A substantially pure protein encoded by the polynucleotide of (8).
(10) An antibody against the protein or peptide of any one of (6), (7), and (9).
(11) A vector comprising the polynucleotide of (5) or (8).

(12) A transformant carrying the polynucleotide of (5) or (8), or the vector of (11).
(13) A transformant expressively carrying the polynucleotide of (5) or (8), or the vector of (11).
(14) A method for producing the protein or peptide of any one of (6), (7), and (9), comprising culturing the transformant of (13) and recovering the expression product.
(15) An oligonucleotide comprising; the nucleotide sequence set forth in any one of the SEQ ID NOs in Table 370 or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.
(16) Use of the oligonucleotide of (15) as a primer for synthesizing a polynucleotide.
(17) Use of the oligonucleotide of (15) as a probe for detecting a gene.
(18) An antisense polynucleotide against the polynucleotide of (8), or the portion thereof.
(19) A method for synthesizing a polynucleotide, the method comprising:

a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of (2) or (3), or the primer of (16); and
b) recovering the synthesized product.

(20) The method of (19), wherein the cDNA library is obtainable by oligo-capping method.
(21) The method of (19), wherein the complementary strand is obtainable by PCR.
(22) A method for detecting the polynucleotide of (8), the method comprising:

a) incubating a target polynucleotide with the oligonucleotide of (15) under the conditions where hybridization occurs, and
b) detecting the hybridization of the target polynucleotide with the oligonucleotide of (15).

(23) A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Table 370 and/or the amino acid sequences set forth in the SEQ ID NOs in Table 370, or a medium on which the database is stored.

[0020] Any patents, patent applications, and publications cited herein are incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0021]

Figure 1 shows the restriction maps of vectors pME18SFL3 and pUC19FL3.
Figure 2 shows the reproducibility of gene expression analysis. The ordinate and the abscissa show the intensities of gene expression obtained in experiments different from each other.
Figure 3 shows the detection limit in gene expression analysis. The intensity of expression is shown in the ordinate, and the concentration (μg/ml) of the probe used is shown in the abscissa.

DETAILED DESCRIPTION OF THE INVENTION

[0022] Herein, "polynucleotide" is defined as a molecule in which multiple nucleotides are polymerized. There are no limitations in the number of the polymerized nucleotides. In case that the polymer contains relatively low number of nucleotides, it is also described as an "oligonucleotide". The polynucleotide or the oligonucleotide of the present invention can be a natural or chemically synthesized product. Alternatively, it can be synthesized using a template DNA by an enzymatic reaction such as PCR.
[0023] All the cDNA provided by the invention are full-length cDNA. Herein, a "full-length cDNA" is defined as a cDNA which contains both ATG codon (the translation start site) and the stop codon. Accordingly, the untranslated regions, which are originally found in the upstream or downstream of the protein coding region in natural mRNA, may or may not be contained.
An "isolated polynucleotide" is a polynucleotide the structure of which is not identical to that of any naturally occurring nucleic acid or to that of any fragment of a naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example,

(a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule but is not flanked by both of the coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs;

(b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA;
(c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and
(d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein. Specifically excluded from this definition are nucleic acids present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones: e.g., as these occur in a DNA library such as a cDNA or genomic DNA library.

[0024] The term "substantially pure" as used herein in reference to a given polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. The substantially pure protein or polypeptide is at least 75% (e.g., at least 80, 85, 95, or 99%) pure by dry weight. Purity can be measured by any appropriate standard method, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.
[0025] All the clones of the present invention (830 clones) are novel and covering full-length, and also predicted to encode any of the following functional protein:

secretory proteins,
membrane proteins,
proteins associated to signal transduction (signal transduction-associated proteins; e.g. protein kinases, etc.),
proteins associated to a glycoprotein (glycoprotein-associated proteins),
proteins associated with transcription (transcription-associated proteins),
proteins associated with diseases (disease-associated proteins),
or, enzymes and/or metabolism-associated proteins, cell division- and/or cell proliferation-associated proteins, cytoskeleton-associated proteins, nuclear proteins, DNA-and/or RNA-binding proteins, ATP- and/or GTP-binding proteins, protein synthesis- and/or protein transport-associated proteins, and cellular defense-associated proteins.

[0026] Furthermore, all the cDNA clones of the present invention can be characterized as follows:

(1) a cDNA that is obtained by the oligo-capping method, which provides cDNA with high fullness ratio. The cDNA was selected by the score in the ATGpr (described as ATGpr1, as well), which is a program for prediction of the fullness of the 5'-end of cDNA based on the features of the 5'-end sequence. In addition, the PSORT, which is a program for prediction of the existence of the signal sequence selected, cDNA that contains a signal sequence in the 5'-end, or transmembrane region in the protein coding region. Furthermore, the homology search with the 5'-end sequences confirmed that, the selected clones were not identical to any of the known human mRNA (namely novel);
or,
(2) a cDNA that is obtained by the oligo-capping method, which provides cDNA with high fullness ratio. The cDNA was selected by the score in the ATGpr, which is a program for prediction of the fullness of the 5'-end based on the features of the 5'-end sequence. Furthermore, the a cDNA that has relative homology with an amino acid sequence of a protein with known functions was selected by the BLAST search (Altschul S.F., Gish W., Miller W., Myers E.W., and Lipman D.J. (1990) J. Mol. Biol. 215: 403-410 ; Gish W., and States D.J. (1993) Nature Genet. 3: 266-272) on the SwissProt database using the 5'-end sequence. In addition, the homology search using the 5'-end sequence confirmed that the selected clones were not identical to any of the known human mRNA (namely novel).

[0027] All clones are obtainable as a full-length clone by such a method as PCR (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4) using both the 5'- and 3'-end sequences, or using the 5'-end sequence and an oligo-dT primer that corresponds to the polyA sequence.
[0028] Specifically, PCR can be performed using an oligonucleotide that has 15 nucleotides longer, and specifically hybridizes with the complementary strand of the polynucleotide that contains the nucleotide sequence selected from the 5'-end sequences shown in Table 1 (SEQ ID NO: 1-829, and SEQ ID NO: 2545), and an oligo-dT primer as a 5'-, and 3'-primer, respectively. The length of the primers is usually 15-100 bp, and favorably between 15-35 bp. In case of LA PCR, which is described below, the primer length of 25-35 bp may provide a good result.
[0029] A method to design a primer that enables a specific amplification based on the given nucleotide sequence is known to those skilled in the art (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4). In designing a primer based on the 5'-end sequence, the primer is designed so as that, in principle, the amplification products will include the translation start site. Accordingly, in case that a given 5'-end nucleotide sequence is the 5'-untranslated region (5'UTR), any part of the sequence can be used as a 5'-primer as far as the specificity toward the target cDNA is insured. The translation start site can be predicted using a known method such

as the ATGpr as described below.

[0030] When synthesizing a polynucleotide, the target nucleotide sequence to be amplified can extend to several thousand bp in some cDNA. However, it is possible to amplify such a long nucleotides by using such as LA PCR (Long and Accurate PCR). It is advantageous to use LA PCR when synthesizing long DNA In LA PCR, in which a special DNA polymerase having 3' □5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, it is reported that amplification of a nucleotide with 20 kb longer can be achieved under desirable condition (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

[0031] A template DNA for synthesizing the cDNA of the present invention can be obtained by using cDNA libraries that are prepared by various methods. The full-length cDNA clones obtained here are those with high fullness ratio, which were obtained using a combination of (1) a method to prepare a full-length-enriched cDNA library using the oligo-capping method, and (2) an estimation system for fullness using the 5'-end sequence (selection based on the estimation by the ATGpr after removing clones that are non-full-length compared to the ESTs). However, it is possible to easily obtain a full-length cDNA by using the primers that are provided by the present invention, not by the above described specialized method.

[0032] The problem with the cDNA libraries prepared by the known methods or commercially available is that mRNA contained in the libraries has very low fullness ratio. Thus, it is difficult to screen full-length cDNA clone directly from the library using ordinary cloning methods. The present invention has revealed a primer that is capable of synthesizing a full-length cDNA. If provided with primers, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods such as oligo-capping, is desirable to synthesize a full-length cDNA with more reliability.

[0033] Once the nucleotide sequences of the full-length cDNAs obtained in the present invention is determined, it is possible to predict the functions of the proteins encoded by the cDNA clones, for example, by searching the databases such as GenBank (http://www.ncbi.nlm.nih.gov/web/GenBank/), Swiss-Prot (http://www.ebi.ac.uk/ebi_docs/Swiss-Prot_db/swisshome.html), UniGene (http://www.ncbi.nlm.nih.gov/UniGene) for homologies of the cDNAs. or by searching the amino acid sequences deduced from the full-length nucleotide sequences for signal sequence by using software such as PSORT (K. Nakai & M. Kanehisa, Genomics, 14: 897-991 (1992), for transmembrane region by using software such as SOSUI (T. Hirokawa et al., Bioinformatics, 14:378-379 (1998); Mitsui Knowledge Industry Co., Ltd.) or for motif by using software such as Pfam (http://www.sanger.ac.uk/Software/Pfam/index.shtml) or PROSITE (http://www.expasy.ch/prosite). As a matter of course, the functions are often predictable by using partial sequence information (preferably 300 nucleotides or more) instead of the full-length nucleotide sequences. However, the result of the prediction obtained by using partial sequence information does not always agree with the result obtained by using full-length nucleotide sequence, and thus it is needless to say that the prediction of function is preferably performed based on the full-length nucleotide sequences.

[0034] Homology search using each of GenBank, Swiss-Prot and UniGene was performed for the 826 clones whose full-length nucleotide sequences had been determined (HEMBA1005337, NT2RM1000407, NT2RM2001767, and NT2RP3003939 are not full-length). The amino acid sequences deduced from the full-length nucleotide sequences were searched for functional domains by using analytical software programs, PSORT, SOSUI and Pfam. Based on the results, proteins encoded by the cDNA clones were grouped into some categories and their functions were predicted.

[0035] The following 437 clones were categorized into secretory and/or membrane proteins. The clones categorized into secretory and/or membrane proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "growth factor", "cytokine", "hormone", "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel", "cell adhesion", "collagen" or "connective tissue"; those which matched the data, suggesting that the proteins are secretory and/or membrane proteins; or those which matched with the full-length sequences of GenBank or UniGene database similar description; and, further, those predicted to have an N-terminal signal sequence or a transmembrane region as a result of domain search for the amino acid sequences deduced from the full-length nucleotide sequences.

BNGH41000020,	BNGH41000087,	BNGH41000091,	HEMBA1000121,	HEMBA1000128,	HEMBA1000349,
HEMBA1000477,	HEMBA1000590,	HEMBA1000713,	HEMBA1000732,	HEMBA1000745,	HEMBA1000835,
HEMBA1000940,	HEMBA1000962,	HEMBA1001221,	HEMBA1001228,	HEMBA1001621,	HEMBA1002131,
HEMBA1002163,	HEMBA1002167,	HEMBA1002178,	HEMBA1002195,	HEMBA1002227,	HEMBA1002420,
HEMBA1002421,	HEMBA1002767,	HEMBA1003047,	HEMBA1003101,	HEMBA1003230,	HEMBA1003392,
HEMBA1003530,	HEMBA1003602,	HEMBA1003732,	HEMBA1003945,	HEMBA1004110,	HEMBA1004250,
HEMBA1004391,	HEMBA1004444,	HEMBA1004454,	HEMBA1004505,	HEMBA1004797,	HEMBA1004982,
HEMBA1005070,	HEMBA1005449,	HEMBA1005522,	HEMBA1005545,	HEMBA1005698,	HEMBA1005945,
HEMBA1006171,	HEMBA1006299,	HEMBA1006311,	HEMBA1006335,	HEMBA1006357,	HEMBA1006430,
HEMBA1006482,	HEMBA1006707,	HEMBA1006724,	HEMBA1006749,	HEMBA1006902,	HEMBA1006960,
HEMBA1007241,	HEMBB1000407,	HEMBB1000447,	HEMBB1000567,	HEMBB1000679,	HEMBB1000881,

HEMBB1001026, HEMBB1001048, HEMBB1001407, HEMBB1001530, HEMBB1001573, HEMBB1001847, HEMBB1001978, HEMBB1002041, HEMBB1002162, HEMBB1002245, HEMBB1002427, HEMBB1002693, MAMMA1000102, MAMMA1000106, MAMMA1000118, MAMMA1000141, MAMMA1000204, MAMMA1000226, MAMMA1000457, MAMMA1000473, MAMMA1000496, MAMMA1000591, MAMMA1000681, MAMMA1000810, MAMMA1000986, MAMMA1000994, MAMMA1001043, MAMMA1001141, MAMMA1001237, MAMMA1001344, MAMMA1001418, MAMMA1001893, MAMMA1001957, MAMMA1001978, MAMMA1002070, MAMMA1002091, MAMMA1002095, MAMMA1002165, MAMMA1002234, MAMMA1002586, MAMMA1002633, MAMMA1003126, NT2RM1000462, NT2RM1000542, NT2RM1000580, NT2RM1000855, NT2RM1000858, NT2RM1000899, NT2RM2000241, NT2RM2000410, NT2RM2000423, NT2RM2000565, NT2RM2001626, NT2RM2001792, NT2RM2001939, NT2RM2001941, NT2RM4000198, NT2RM4000284, NT2RM4000417, NT2RM4000444, NT2RM4000587, NT2RM4000593, NT2RM4000648, NT2RM4000761, NT2RM4000997, NT2RM4001325, NT2RM4001735, NT2RM4001768, NT2RM4001843, NT2RM4002352, NT2RP1000050, NT2RP1000181, NT2RP1000261, NT2RP1000300, NT2RP1000325, NT2RP1000448, NT2RP1000551, NT2RP1000613, NT2RP1000981, NT2RP1001004, NT2RP1001563, NT2RP2000479, NT2RP2000533, NT2RP2000616, NT2RP2000649, NT2RP2000663, NT2RP2000694, NT2RP2000818, NT2RP2000903, NT2RP2001200, NT2RP2001276, NT2RP2001480, NT2RP2001495, NT2RP2001514, NT2RP2001755, NT2RP2001915, NT2RP2001956, NT2RP2002063, NT2RP2002188, NT2RP2002232, NT2RP2002527, NT2RP2002533, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002976, NT2RP2003042, NT2RP2003210, NT2RP2003383, NT2RP2003390, NT2RP2003469, NT2RP2003593, NT2RP2003655, NT2RP2003664, NT2RP2003950, NT2RP2004179, NT2RP2004205, NT2RP2004495, NT2RP2004524, NT2RP2004556, NT2RP2004606, NT2RP2004648, NT2RP2004794, NT2RP2005027, NT2RP2005163, NT2RP2005181, NT2RP2005378, NT2RP2005463, NT2RP2005541, NT2RP2005597, NT2RP2005666, NT2RP2005883, NT2RP2005994, NT2RP2006004, NT2RP2006042, NT2RP2006269, NT2RP1006512, NT2RP2006580, NT2RP3000169, NT2RP3000171, NT2RP3000304, NT2RP3000436, NT2RP3000460, NT2RP3000616, NT2RP3000676, NT2RP3000721, NT2RP3000818, NT2RP3000907, NT2RP3000921, NT2RP3001012, NT2RP3001159, NT2RP3001195, NT2RP3001240, NT2RP3001271, NT2RP3001322, NT2RP3001388, NT2RP3001560, NT2RP3001592, NT2RP3001650, NT2RP3001738, NT2RP3001858, NT2RP3002015, NT2RP3002160, NT2RP3002311, NT2RP3002342, NT2RP3002411, NT2RP3002737, NT2RP3002790, NT2RP3002836, NT2RP3002900, NT2RP3002958, NT2RP3003000, NT2RP3003076, NT2RP3003354, NT2RP3003532, NT2RP3003535, NT2RP3003614, NT2RP3004025, NT2RP3004075, NT2RP3004083, NT2RP3004130, NT2RP3004133, NT2RP3004309, NT2RP3004345, NT2RP3004406, NT2RP3004481, NT2RP3004552, NT2RP3004625, NT2RP3004647, NT2RP4001001, NT2RP4001009, NT2RP4001467, NT2RP4001879, NT2RP4002187, NT2RP4002451, NT2RP4002750, OVARC1000003, OVARC1000105, OVARC1000298, OVARC1000307, OVARC1000313, OVARC1000410, OVARC1000439, OVARC1000553, OVARC1000811, OVARC1000873, OVARC1000956, OVARC1001030, OVARC1001163, OVARC1001336, OVARC1001570, OVARC1001607, OVARC1001725, OVARC1001991, PLACE1000033, PLACE1000231, PLACE1000560, PLACE1000740, PLACE1000912, PLACE1000914, PLACE1000927, PLACE1001016, PLACE1001123, PLACE1001183, PLACE1001231, PLACE1001340, PLACE1001401, PLACE1001407, PLACE1001464, PLACE1001516, PLACE1001536, PLACE1001564, PLACE1001655, PLACE1001795, PLACE1001836, PLACE1001918, PLACE1001949, PLACE1002080, PLACE1002095, PLACE1002355, PLACE1002374, PLACE1002518, PLACE1002547, PLACE1002726, PLACE1002905, PLACE1002911, PLACE1002967, PLACE1003407, PLACE1003573, PLACE1003737, PLACE1003772, PLACE1003839, PLACE1003845, PLACE1003852, PLACE1004279, PLACE1004282, PLACE1004441, PLACE1004450, PLACE1004482, PLACE1004520, PLACE1004630, PLACE1004657, PLACE1004648, PLACE1004816, PLACE1005003, PLACE1005005, PLACE1005031, PLACE1005383, PLACE1005410, PLACE1005426, PLACE1005544, PLACE1005569, PLACE1005660, PLACE1005725, PLACE1005745, PLACE1005878, PLACE1005927, PLACE1006071, PLACE1006093, PLACE1006208, PLACE1006277, PLACE1006290, PLACE1006443, PLACE1006716, PLACE1006809, PLACE1006959, PLACE1007081, PLACE1007096, PLACE1007296, PLACE1007626, PLACE1007845, PLACE1007881, PLACE1008359, PLACE1008469, PLACE1008716, PLACE1008744, PLACE1008985, PLACE1009067, PLACE1009196, PLACE1009279, PLACE1009527, PLACE1009546, PLACE1009600, PLACE1009982, PLACE1010011, PLACE1010078, PLACE1010251, PLACE1010445, PLACE1010713, PLACE1010784, PLACE1010827, PLACE1010968, PLACE1011116, PLACE1011181, PLACE1011236, PLACE1011516, PLACE1011708, PLACE3000181, PLACE3000213, PLACE4000354, SKNMC1000004, SKNMC1000014, SKNMC1000082, THYRO1000036, THYRO1000099, THYRO1000196, THYRO1000400, THYRO1000584, THYRO1000678, THYRO1000776, THYRO1000795, THYRO1000956, THYRO1001102, THYRO1001113, THYRO1001205, THYRO1001237, THYRO1001242, THYRO1001266, THYRO1001327, THYRO1001456,

THYRO1001478, THYRO1001523, THYRO1001529, THYRO1001641, THYRO1001702, THYRO1001725, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1000426, Y79AA1000521, Y79AA1000876, Y79AA1000888, Y79AA1000959, Y79AA1001013, Y79AA1001212, Y79AA1001264, Y79AA1001328, Y79AA1001426, Y79AA1001427, Y79AA1001430, Y79AA1001727, Y79AA1001787, Y79AA1001795, Y79AA1001799, Y79AA1001803, Y79AA1002022, Y79AA1002058, Y79AA1002129, Y79AA1002213, Y79AA1002373,

[0036] The following 146 clones were categorized into glycoprotein-associated proteins. The clones categorized into glycoprotein-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keyword "glycoprotein"; those which matched the data suggesting that the proteins are glycoprotein; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

BNGH41000087, BNGH41000091, HEMBA1000349, HEMBA1000590, HEMBA1000745, HEMBA1000835, HEMBA1001221, HEMBA1001228, HEMBA1001621, HEMBA1002131, HEMBA1002178, HEMBA1002421, HEMBA1002767, HEMBA1003230, HEMBA1003392, HEMBA1004250, HEMBA1004391, HEMBA1004444, HEMBA1004505, HEMBA1005449, HEMBA1005522, HEMBA1005545, HEMBA1006707, HEMBA1006749, HEMBA1006902, HEMBB1000679, HEMBB1000881, HEMBB1001048, HEMBB1002120, HEMBB1002245, HEMBB1002427, MAMMA1000102, MAMMA1000591, MAMMA1000681, MAMMA1001043, MAMMA1001237, MAMMA1002070, MAMMA1002586, MAMMA1003126, NT2RM1000462, NT2RM1000580, NT2RM2001792, NT2RM2001818, NT2RM2001939, NT2RM2001941, NT2RM4000198, NT2RM4000284, NT2RM4000417, NT2RM4000648, NT2RM4000997, NT2RM4001325, NT2RM4002352, NT2RP1000613, NT2RP1000981, NT2RP1001004, NT2RP2000616, NT2RP2000694, NT2RP2000903, NT2RP2001480, NT2RP2001755, NT2RP2002533, NT2RP2003042, NT2RP2003210, NT2RP2004205, NT2RP2004606, NT2RP2005027, NT2RP2005181, NT2RP2005541, NT2RP2005597, NT2RP2005883, NT2RP2006004, NT2RP2006042, NT2RP2006269, NT2RP3000304, NT2RP3000616, NT2RP3000921, NT2RP3001650, NT2RP3002160, NT2RP3002737, NT2RP3002958, NT2RP3003000, NT2RP3003532, NT2RP3004130, NT2RP3004133, NT2RP3004481, NT2RP3004552, NT2RP3004640, NT2RP4000108, NT2RP4001467, NT2RP4002750, OVARC1000003, OVARC1000553, OVARC1000811, OVARC1000873, OVARC1001336, OVARC1001607, OVARC1001991, PLACE1000033, PLACE1000740, PLACE1001016, PLACE1001123, PLACE1001231, PLACE1001464, PLACE1001655, PLACE1001836, PLACE1002355, PLACE1002374, PLACE1002905, PLACE1002911, PLACE1003573, PLACE1003737, PLACE1003772, PLACE1003839, PLACE1004282, PLACE1004441, PLACE1004450, PLACE1004520, PLACE1004648, PLACE1005003, PLACE1005426, PLACE1006071, PLACE1006073, PLACE1006290, PLACE1007081, PLACE1007845, PLACE1008716, PLACE1008744, PLACE1008985, PLACE1010251, PLACE1010784, PLACE1010968, PLACE1011116, PLACE3000181, PLACE3000213, PLACE4000354, THYRO1000036, THYRO1000196, THYRO1000584, THYRO1000956, THYRO1001266, Y79AA1000270, Y79AA1000426, Y79AA1001727, Y79AA1001795, Y79AA1002022, Y79AA1002213,

[0037] The following 57 clones were categorized into signal transduction-associated proteins. The clones categorized into signal transduction-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "serine/threonine-protein kinase", "tyrosine-protein kinase" or "SH3 domain"; those which matched the data suggesting that the proteins are signal transduction-associated proteins (for example, "ADP-ribosylation factor"); or those which matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those which was similarly predicted to be signal transduction-associated proteins based on the matching data of Pfam.

HEMBA1000006, HEMBA1002195, HEMBA1002227, HEMBA1002551, HEMBA1005084, HEMBA1005929, HEMBA1006658, HEMBA1006916, MAMMA1000881, MAMMA1001150, MAMMA1001310, MAMMA1002142, NT2RM2001902, NT2RP1001020, NT2RP1001031, NT2RP2001469, NT2RP2001529, NT2RP2001769, NT2RP2003179, NT2RP2003545, NT2RP2004670, NT2RP3000011, NT2RP3000022, NT2RP3000172, NT2RP3000201, NT2RP3000820, NT2RP3003527, NT2RP3003849, NT2RP3003874, NT2RP3004067, NT2RP4000634, NT2RP4000962, OVARC1000255, OVARC1000529, OVARC1000916, OVARC1001338, OVARC1001569, PLACE1002329, PLACE1003135, PLACE1003598, PLACE1005519, PLACE1006208, PLACE1008282, PLACE1008297, PLACE1010081, PLACE1011364, PLACE1011824, THYRO1001457, THYRO1001593, THYRO1001700, THYRO1001770, Y79AA1000777, Y79AA1000967, Y79AA1002376, Y79AA1002381, HEMBB1000668, NT2RM4001377

[0038] The following 81 clones were categorized into transcription-associated proteins. The clones categorized into transcription-associated proteins are those which keywords "transcription regulation", "zinc finger" or "homeobox" matched the full-length sequences of Swiss-Prot database; those which the matched the data suggesting that the proteins were transcription-associated proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those which was similarly predicted to be transcription-associated proteins based on the matching data of Pfam.

HEMBA1000462, HEMBA1000671, HEMBA1001297, HEMBA1001390, HEMBA1001886, HEMBA1002048, HEMBA1003120, HEMBA1003497, HEMBA1004785, HEMBA1005230, HEMBA1005246, HEMBA1006276, HEMBA1006572, HEMBA1007226, HEMBB1000106, HEMBB1000905, HEMBB1001959, HEMBB1002051, HEMBB1002661, MAMMA1001094, MAMMA1001532, MAMMA1001615, NT2RM1000789, NT2RM2000632, NT2RM2000773, NT2RM4000326, NT2RP1000271, NT2RP1000468, NT2RP2000092, NT2RP2000610, NT2RP2000712, NT2RP2000739, NT2RP2001538, NT2RP2001662, NT2RP2001817, NT2RP2001948, NT2RP2002564, NT2RP2002974, NT2RP2003138, NT2RP2003302, NT2RP2003940, NT2RP2004108, NT2RP2004847, NT2RP2005247, NT2RP2005391, NT2RP2005535, NT2RP2005774, NT2RP2005941, NT2RP2006092, NT2RP3000148, NT2RP3000232, NT2RP3000378, NT2RP3000652, NT2RP3001976, NT2RP3004090, NT2RP3004119, NT2RP3004294, OVARC1001049, OVARC1001086, OVARC1001132, OVARC1001807, PLACE1000258, PLACE1000442, PLACE1000907, PLACE1003529, PLACE1004166, PLACE1004168, PLACE1004887, PLACE1005250, PLACE1005682, PLACE1006079, PLACE1008549, PLACE1011407, PLACE1011978, THYRO1000580, Y79AA1000030, Y79AA1001090, Y79AA1001523, Y79AA1002334, Y79AA1002378, HEMBB1002302,

[0039] The following 85 clones were categorized into disease-associated proteins. The clones categorized into disease-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "disease mutation" or "syndrome"; those which matched the data suggesting that the proteins are disease-associated proteins; or those which matched the full-length sequences of Swiss-Prot database and GenBank or UniGene database where the matched sequences are those of genes or proteins which had been deposited in the database of Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is a database of human genes and diseases.

BNGH41000020, HEMBA1000349, HEMBA1000590, HEMBA1000671, HEMBA1000835, HEMBA1001184, HEMBA1001228, HEMBA1001886, HEMBA1003120, HEMBA1004250, HEMBA1005246, HEMBA1005267, HEMBA1006707, HEMBA1006749, HEMBA1006902, HEMBA1006916, HEMBA1007013, HEMBB1002120, MAMMA1000204, MAMMA1002080, NT2RM2000632, NT2RM2001126, NT2RM2001558, NT2RP1000271, NT2RP1000465, NT2RP1000579, NT2RP2000447, NT2RP2000514, NT2RP2000739, NT2RP2001223, NT2RP2001529, NT2RP2001562, NT2RP2002674, NT2RP2003369, NT2RP2004108, NT2RP2004205, NT2RP2005535, NT2RP2005941, NT2RP2006004, NT2RP3000059, NT2RP3000125, NT2RP3000201, NT2RP3000232, NT2RP3000616, NT2RP3000677, NT2RP3000838, NT2RP3000921, NT2RP3001542, NT2RP3002286, NT2RP3002721, NT2RP3002737, NT2RP3002738, NT2RP3004481, OVARC1000208, OVARC1000275, OVARC1000331, OVARC1000410, OVARC1001086, OVARC1001132, OVARC1001607, OVARC1001725, OVARC1001952, PLACE1000258, PLACE1000442, PLACE1000907, PLACE1001100, PLACE1001500, PLACE1002905, PLACE1002967, PLACE1003407, PLACE1003428, PLACE1005005, PLACE1005239, PLACE1005815, PLACE1007028, PLACE1008716, PLACE1011407, PLACE1011978, PLACE2000118, THYPO1000580, THYRO1000866, THYRO1001071, THYRO1001478, Y79AA1001062, Y79AA1001530,

[0040] It is unclear, by the analyses so far, whether or not the remaining 212 clones encode proteins belonging to any of the categories of secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins or disease-associated proteins. Nonetheless, it is still possible for these clones to encode secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, or disease-associated proteins. On the other hand, some of these clones can be presumed to have functions other than those as secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins and disease-associated proteins.

[0041] Among the 212 clones, the following clones presumably belong to the categories of enzymes and/or metabolism-associated proteins, cell division- and/or cell proliferation-associated proteins, cytoskeleton-associated proteins, nuclear proteins, DNA- and/or RNA-binding proteins, ATP-and/or GTP-binding proteins, protein synthesis- and/or protein transport-associated proteins, or cellular defense-associated proteins, although it is unclear whether or not the clones belong to any of the categories of secretory and/or transmembrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, and disease-associated proteins.

[0042] The following 10 clones presumably belong to the category of enzymes and/or metabolism-associated proteins. The clones herein defined as clones presumably belonging to the category of enzymes and/or metabolism-associated proteins matched data containing keywords such as "metabolism", "oxidoreductase" and "E.C. No. (Enzyme commission number)".

HEMBA1003315, HEMBB1002465, MAMMA1000614, NT2RP2000178, NT2RP2001388, NT2RP2001903, NT2RP2002304, NT2RP2005878, NT2RP3001685, PLACE1006219

[0043] The following 4 clones presumably belong to the category of cell division- and/or cell proliferation-associated proteins. The cDNA clones were herein defined as clones presumably belonging to the category of cell division- and/

or cell proliferation-associated proteins matched data containing keywords such as "cell division", "cell cycle", "mitosis", "chromosomal protein", "cell growth" and "apoptosis".

MAMMA1000403, NT2RM2000497, NT2RP2000394, Y79AA1002121

[0044] The following 6 clones presumably belong to the category of cytoskeleton-associated proteins. The cDNA clones were herein defined as clones presumably belonging to the category of cytoskeleton-associated proteins matched data containing keywords such as "structural protein", "cytoskeleton", "actin-binding" and "microtubules".

MAMMA 1001609, NT2RM2000589, NT2RP3000063, PLACE 1004078, PLACE 1004492, PLACE 1008657

[0045] The following 7 clones presumably belong to the category of nuclear proteins. The cDNA clones were herein defined as clones presumably belonging to the category of nuclear proteins matched data containing keywords such as "nuclear protein".

HEMBA1001878, HEMBA1002992, MAMMA1000614, NT2RM4000965, NT2RM2001738, NT2RP2001388, Y79AA1002121

[0046] The following 5 clones presumably belong to the category of DNA- and/or RNA-binding proteins. The cDNA clones were herein defined as clones presumably belonging to the category of DNA- and/or RNA-binding proteins matched data containing keywords such as "DNA-binding" and "RNA-binding".

HEMBA1003072, HEMBA1006770, HEMBA1007332, NT2RM2000497, Y79AA1002121

[0047] The following 7 clones presumably belong to the category of ATP- and/or GTP-binding proteins. The cDNA clones were herein defined as clones presumably belonging to the category of ATP- and/or GTP-binding proteins matched data containing keywords such as "ATP-binding" and "GTP-binding".

HEMBA1002316, MAMMA1001609, NT2RM2000306, NT2RM2000497, NT2RP2000178, NT2RP3003729, PLACE1004305

[0048] The following 7 clones presumably belong to the category of protein synthesis- and/or protein transport-associated proteins. The cDNA clones were herein defined as clones presumably belonging to the category of protein synthesis-associated and/or protein transport-associated proteins matched data containing keywords such as "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", "protein transport" and "signal recognition particle".

NT2RM4000965, NT2RP2005069, NT2RP3000481, NT2RP3000789, NT2RP4001877, OVARC1001833, OVARC1002058,

[0049] The following 1 clone presumably belongs to the category of cellular defense-associated proteins. The cDNA clones were herein defined as clones presumably belonging to the category of cellular defense-associated proteins matched data containing keywords such as "heat shock", "DNA repair" and "DNA damage".

PLACE1005539

[0050] Although it is unclear whether or not 26 out of 174 clones other than the above-mentioned clones belong to any of the above-described categories, these clones are predicted to have some functions, based on the homology search using their full-length sequences thereof. The clone names and the gene definitions found in the result of homology search are shown below, separated with a double-slash mark, //.

HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.
HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.
HEMBA1003399//MVP1 PROTEIN.
HEMBA1005489//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.
HEMBB1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.
MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds.
MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.
NT2RM2000514//Homo Sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.
NT2RM2000622//Mus musculus F-box protein FBL10 mRNA, partial cds.
NT2RM4000100//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.
NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.
NT2RP3001170//Mus musculus activity-dependent neuroprotective protein (Adnp) mRNA, complete cds.
NT2RP3002571//Bos taurus mRNA for lyncein.
NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.
OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds.
PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.
PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.
PLACE1005736//Human mRNA for BAS-GRIP protein.
PLACE1007702//Mus musculus TRA1 mRNA, complete cds.
PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.

THYRO1000061//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.
THYRO1000964//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.
Y79AA1000776//Mus musculus mRNA for GSG1, complete cds.
Y79AA1001056//Homo sapiens MAID protein mRNA, complete cds.
Y79AA1001272//Homo sapiens retinoic acid repressible protein (RARG-1) mRNA, complete cds.
Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.

[0051] So far, useful information for presuming the functions are unavailable for the remaining 148 clones, whose names are listed below.

HEMBA1000275, HEMBA1000300, HEMBA1000443, HEMBA1000875, HEMBA1000907, HEMBA1001272, HEMBA1001296, HEMBA1001563, HEMBA1002164, HEMBA1002239, HEMBA1002985, HEMBA1003294, HEMBA1003487, HEMBA1004007, HEMBA1004067, HEMBA1004085, HEMBA1004952, HEMBA1004971, HEMBA1005145, HEMBA1005430, HEMBA1005913, HEMBA1006016, HEMBA1006517, HEMBA1006544, HEMBA1006912, HEMBA1007057, HEMBA1007063, HEMBA1007291, HEMBB1000276, HEMBB1000309, HEMBB1000642, HEMBB1001200, HEMBB1001547, HEMBB1002039, HEMBB1002228, HEMBB1002663, MAMMA1000046, MAMMA1000449, MAMMA1000528, MAMMA1000652, MAMMA1000706, MAMMA1000814, MAMMA1001066, MAMMA1001284, MAMMA1001623, MAMMA1001634, MAMMA1001901, MAMMA1002087, MAMMA1002205, MAMMA1002224, NT2RM2000582, NT2RM2001643, NT2RM4000115, NT2RM4000295, NT2RM4001321, NT2RP1000002, NT2RP1000239, NT2RP1000679, NT2RP1000740, NT2RP1000903, NT2RP2000240, NT2RP2001878, NT2RP2001921, NT2RP2002015, NT2RP2002409, NT2RP2002510, NT2RP2003599, NT2RP2003931, NT2RP2004069, NT2RP2004141, NT2RP2004447, NT2RP2004837, NT2RP2005514, NT2RP2005632, NT2RP2005887, NT2RP2006099, NT2RP2006134, NT2RP3000427, NT2RP3000444, NT2RP3000645, NT2RP3000871, NT2RP3001044, NT2RP3001061, NT2RP3001754, NT2RP3002281, NT2RP3002324, NT2RP3002353, NT2RP3002409, NT2RP3002448, NT2RP3002664, NT2RP3002887, NT2RP3002983, NT2RP3003448, NT2RP3003469, NT2RP3003473, NT2RP3003559, NT2RP3003963, NT2RP3004000, NT2RP3004202, NT2RP3004321, NT2RP3004355, NT2RP3004374, NT2RP4002715, OVARC1000090, OVARC1000137, OVARC1000467, OVARC1000775, OVARC1000853, OVARC1000995, OVARC1001222, OVARC1001260, OVARC1001727, OVARC1002178, PLACE1000986, PLACE1001114, PLACE1001229, PLACE1001788, PLACE1003438, PLACE1003460, PLACE1003644, PLACE1004028, PLACE1004199, PLACE1004519, PLACE1005601, PLACE1005669, PLACE1005768, PLACE1006515, PLACE1006786, PLACE1007040, PLACE1007077, PLACE1007591, PLACE1007971, PLACE1008984, PLACE1009735, PLACE2000219, PLACE4000455, THYRO1000846, THYRO1000999, THYRO1001063, THYRO1001128, THYRO1001471, THYRO1001495, THYRO1001608, THYRO1001803, Y79AA1000127, Y79AA1000750, Y79AA1001592, Y79AA1001863,

[0052] In the 437 clones categorized into secretory and/or membrane proteins by using their full-length sequences, 410 clones were also predicted to encode proteins having functions of secretory and/or membrane proteins by using their partial nucleotide sequences. In the 146 clones categorized into glycoprotein-associated proteins by using their full-length sequences, 124 clones were also predicted to encode proteins having functions of glycoprotein-associated proteins by using their partial nucleotide sequences. In the 57 clones categorized into signal transduction-associated proteins by using their full-length sequences, 46 clones were also predicted to encode proteins having functions of signal transduction-associated proteins by using their partial nucleotide sequences. In the 81 clones categorized into transcription-associated proteins by using their full-length sequences, 57 clones were also predicted to encode proteins having functions of transcription-associated proteins by using their partial nucleotide sequences. In the 85 clones categorized into disease-associated proteins by using their full-length sequences, 6 clones were also predicted to encode proteins having functions of disease-associated proteins by using their partial nucleotide sequences. The number of clones, which were predicted to encode disease-associated proteins based on the full-length nucleotide sequences, is much greater than that predicted based on the partial sequences. The reason is that the full-length sequences were categorized by using the data found in the OMIM database into the category of disease-associated proteins.

[0053] In some cases, the predicted functions based on the partial sequences are different from those based on the full-length sequences. The reason is that a protein does not always belong solely to a single category of the above-described functional categories, and therefore, it is possible for the protein to belong to both of the predicted functional categories. Besides, additional functions can be found for the clones classified into these functional categories by further analyses.

[0054] The following list shows the cDNA clones predicted and selected on the basis of the partial sequences (5' sequences) as cDNAs encoding secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, or disease-associated proteins.

[0055] The clones that are selected by the score in the ATGpr and by the PSORT for the existence of a signal sequence can be expected to encode a secretory or membrane protein since they are predicted to possess the secretion

signal or a transmembrane region. The clones that are selected by the score in the ATGpr and by the PSORT for the existence of a signal sequence are listed below (254 clones).

HEMBA1000300 HEMBA1000713 HEMBA1000907
HEMBA1000962 HEMBA1001272 HEMBA1001297
HEMBA1002164 HEMBA1002239 HEMBA1002420
HEMBA1002421 HEMBA1003101 HEMBA1003294
HEMBA1003399 HEMBA1003602 HEMBA1003732
HEMBA1004110 HEMBA1004797 HEMBA1005430
HEMBA1006016 HEMBA1006171 HEMBA1006311
HEMBA1006335 HEMBA1006357 HEMBA1006572
HEMBA1006658 HEMBA1006707 HEMBA1006902
HEMBA1006960 HEMBA1007013 HEMBB1000276
HEMBB1000447 HEMBB1000567 HEMBB1000642
HEMBB1000905 HEMBB1001200 HEMBB1001407
HEMBB1001530 HEMBB1001547 HEMBB1001978
HEMBB1002162 HEMBB1002228 HEMBB1002245
HEMBB1002427 HEMBB1002465 HEMBB1002663
HEMBB1002693 MAMMA1000046 MAMMA1000102
MAMMA1000118 MAMMA1000141 MAMMA1000449
MAMMA1000457 MAMMA1000591 MAMMA1000652
MAMMA1000681 MAMMA1000986 MAMMA1000994
MAMMA1001043 MAMMA1001141 MAMMA1001284
MAMMA1001310 MAMMA1001344 MAMMA1001893
MAMMA1001901 MAMMA1001957 MAMMA1002070
MAMMA1002087 MAMMA1002165 MAMMA1002205
MAMMA1002224 MAMMA1002633 NT2RM2000241
NT2RM2000306 NT2RM2000410 NT2RM2000514
NT2RM2001643 NT2RM2001941 NT2RM4000115
NT2RM4000997 NT2RM4001321 NT2RM4001325
NT2RM4001768 NT2RP1000050 NT2RP1000448
NT2RP1000903 NT2RP1001563 NT2RP2000479
NT2RP2001495 NT2RP2001915 NT2RP2001948
NT2RP2002015 NT2RP2002063 NT2RP2002304
NT2RP2002674 NT2RP2002721 NT2RP2003383
NT2RP2003469 NT2RP2003593 NT2RP2003599
NT2RP2003655 NT2RP2003664 NT2RP2004179
NT2RP2004447 NT2RP2004495 NT2RP2004524
NT2RP2004556 NT2RP2004837 NT2RP2005027
NT2RP2005463 NT2RP2005514 NT2RP2005887
NT2RP2006042 NT2RP2006269 NT2RP3000169
NT2RP3000460 NT2RP3000481 NT2RP3000645
NT2RP3000789 NT2RP3000818 NT2RP3001012
NT2RP3001044 NT2RP3001195 NT2RP3001560
NT2RP3001685 NT2RP3001858 NT2RP3002160
NT2RP3002281 NT2RP3002721 N12RP3002836
NT2RP3002958 NT2RP3003076 NT2RP3003354
NT2RP3003469 NT2RP3003535 NT2RP3003559
NT2RP3003963 NT2RP3004000 NT2RP3004083
NT2RP3004133 NT2RP3004309 NT2RP3004321
NT2RP3004355 NT2RP3004374 NT2RP4001001
NT2RP4001879 NT2RP4002451 NT2RP4002715
OVARC1000208 OVARC1000298 OVARC1000439
OVARC1000775 OVARC1000811 OVARC1000853
OVARC1001222 OVARC1001727 OVARC1001807
OVARC1001833 PLACE1000231 PLACE1000560
PLACE1000740 PLACE1000912 PLACE1000914
PLACE1000927 PLACE1000986 PLACE1001100

PLACE1001183 PLACE1001229 PLACE1001407
PLACE1001536 PLACE1001788 PLACE1002080
PLACE1002095 PLACE1002374 PLACE1002518
PLACE1003407 PLACE1003428 PLACE1003460
PLACE1003839 PLACE1003845 PLACE1004028
PLACE1004199 PLACE1004282 PLACE1004305
PLACE1004482 PLACE1004637 PLACE1005005
PLACE1005250 PLACE1005383 PLACE1005410
PLACE1005544 PLACE1005569 PLACE1005601
PLACE1005660 PLACE1005669 PLACE1005725
PLACE1005768 PLACE1005927 PLACE1006079
PLACE1006093 PLACE1006219 PLACE1006277
PLACE1006443 PLACE1006786 PLACE1006809
PLACE1007040 PLACE1007096 PLACE1007296
PLACE1007626 PLACE1007971 PLACE1008469
PLACE1008984 PLACE1008985 PLACE1009067
PLACE1009196 PLACE1009527 PLACE1009982
PLACE1010251 PLACE1011236 PLACE2000219
PLACE4000455 SKNMC1000004 SKNMC1000014
THYRO1000036 THYRO1000099 THYRO1000196
THYRO1000795 THYRO1000999 THYRO1001237
THYRO1001327 THYRO1001478 THYRO1001495
THYRO1001523 THYRO1001702 THYRO1001725
Y79AA1000226 Y79AA1000270 Y79AA1000426
Y79AA1000521 Y79AA1000776 Y79AA1000959
Y79AA1001013 Y79AA1001056 Y79AA1001264
Y79AA1001328 Y79AA1001427 Y79AA1001430
Y79AA1001530 Y79AA1001592 Y79AA1001793
Y79AA1001795 Y79M1001803 Y79AA1001863
Y79AA1002022 Y79AA1002373

[0056] In the example mentioned below, the 254 clones as described above were categorized into three groups according to their maximal value in the ATGpr and the result in the PSORT, which are shown in Table 7-10, 11, 12 (246 clones), and Table 13, 14, 15 (8 clones). In the tables, the name of clone, indicate the name of the clone that was selected by the ATGpr and the PSORT; the name of sequence indicates the name of the 5'-end sequence of the clone on the left; the maximal ATGpr score indicates the maximal ATGpr1 score of the 5'-end sequence shown on the left; and signal indicates the presence of the signal sequence according to the prediction by the PSORT. In addition, the representative sequence is the sequence that has the longest sequence among the cluster in which the 5'-end sequence on the left was included. The maximal ATGpr score and signal on the right indicate the maximal ATGpr1 score of the representative sequence, and the presence of a signal sequence in the representative sequence according to the prediction by the PSORT, respectively. The 170 clones shown in Table 7-10, having the maximal score in the ATGpr1 higher than 0.5, and predicted to possess a signal sequence by the PSORT, are very likely to be full-length and encode a secretory or membrane protein. The 35 clones in Table 11, which have the maximal score in the ATGpr1 0.3 or higher and less than 0.5, and predicted to have a signal sequence, are also as well. And, the 41 clones in Table 12, having the maximal score in the ATGpr1 0 or higher and less than 0.3, and predicted to have a signal sequence, are likely to be full-length and encode a secretory or membrane protein.

[0057] The 8 clones in Table 13 (4 clones), Table 14 (2 clones), and Table 15 (2 clones) have the maximal score in the ATGpr1 0.5 or higher, 0.3 or higher and less than 0.5, and 0 or higher and less than 0.3, respectively, and are predicted to have no signal sequence by the PSORT. However, these clones contain a region that is recognized by the PSORT to be a signal sequence within the representative sequence composing the same cluster. Thus, the clones were judged as a full-length clone which encodes a membrane protein, especially.

[0058] The clones selected by the score in the ATGpr and by the keywords in the top hit data in the SwissProt are likely to encode a secretory or membrane protein, or proteins with functions associated to signal transduction, glycoprotein, transcription, and diseases according to the respective keywords. These 659 clones are shown below. Here, top hit data is defined to be data of known amino acid sequence which is identified to be the most homologous sequence in homology search using the SwissProt.

BNGH41000020 BNGH41000087 BNGH41000091

HEMBA1000006 HEMBA1000121 HEMBN1000128
HEMBA1000275 HEMBA1000349 HEMBA1000443
HEMBA1000462 HEMBA1000477 HEMBA1000590
HEMBA1000634 HEMBA1000671 HEMBA1000732
HEMBA1000745 HEMBA1000835 HEMBA1000875
HEMBA1000907 HEMBA1000940 HEMBA1001184
HEMBA1001221 HEMBA1001228 HEMBA1001296
HEMBA1001390 HEMBA1001563 HEMBA1001621
HEMBA1001878 HEMBA1001886 HEMBA1002048
HEMBA1002131 HEMBA1002163 HEMBA1002164
HEMBA1002167 HEMBA1002178 HEMBA1002195
HEMBA1002227 HEMBA1002316 HEMBA1002421
HEMBA1002524 HEMBA1002551 HEMBA1002767
HEMBA1002985 HEMBA1002992 HEMBA1003047
HEMBA1003072 HEMBA1003101 HEMBA1003120
HEMBA1003230 HEMBA1003315 HEMBA1003392
HEMBA1003487 HEMBA1003497 HEMBA1003530
HEMBA1003945 HEMBA1004007 HEMBA1004067
HEMBA1004085 HEMBA1004250 HEMBA1004391
HEMBA1004444 HEMBA1004454 HEMBA1004505
HEMBA1004785 HEMBA1004797 HEMBA1004952
HEMBA1004971 HEMBA1004982 HEMBA1005070
HEMBA1005084 HEMBA1005145 HEMBA1005230
HEMBA1005246 HEMBA1005267 HEMBA1005337
HEMBA1005449 HEMBA1005489 HEMBA1005522
HEMBA1005545 HEMBA1005698 HEMBA1005913
HEMBA1005929 HEMBA1005945 HEMBA1006276
HEMBA1006299 HEMBA1006335 HEMBA1006430
HEMBA1006482 HEMBA1006517 HEMBA1006544
HEMBA1006572 HEMBA1006707 HEMBA1006724
HEMBA1006749 HEMBA1006770 HEMBA1006902
HEMBA1006912 HEMBA1006916 HEMBA1007013
HEMBA1007057 HEMBA1007063 HEMBA1007226
HEMBA1007241 HEMBA1007291 HEMBA1007332
HEMBB1000106 HEMBB1000309 HEMBB1000407
HEMBB1000447 HEMBB1000542 HEMBB1000567
HEMBB1000668 HEMBB1000679 HEMBB1000881
HEMBB1001026 HEMBB1001048 HEMBB1001200
HEMBB1001573 HEMBB1001847 HEMBB1001959
HEMBB1002039 HEMBB1002041 HEMBB1002051
HEMBB1002120 HEMBB1002302 HEMBB1002427
HEMBB1002661 MAMMA1000106 MAMMA1000204
MAMMA1000226 MAMMA1000403 MAMMA1000473
MAMMA1000496 MAMMA1000528 MAMMA1000591
MAMMA1000614 MAMMA1000681 MAMMA1000706
MAMMA1000788 MAMMA1000810 MAMMA1000814
MAMMA1000881 MAMMA1001043 MAMMA1001066
MAMMA1001094 MAMMA1001150 MAMMA1001237
MAMMA1001418 MAMMA1001532 MAMMA1001609
MAMMA1001615 MAMMA1001623 MAMMA1001634
MAMMA1001893 MAMMA1001957 MAMMA1001978
MAMMA1002070 MAMMA1002080 MAMMA1002091
MAMMA1002095 MAMMA1002128 MAMMA1002142
MAMMA1002165 MAMMA1002234 MAMMA1002586
MAMMA1002633 MAMMA1003126 NT2RM1000407
NT2RM1000462 NT2RM1000542 NT2RM1000580
NT2RM1000789 NT2RM1000855 NT2RM1000858
NT2RM1000899 NT2RM2000410 NT2RM2000423

NT2RM2000497 NT2RM2000565 NT2RM2000582
NT2RM2000589 NT2RM2000622 NT2RM2000632
NT2RM2000773 NT2RM2001126 NT2RM2001558
NT2RM2001626 NT2RM2001738 NT2RM2001767
NT2RM2001792 NT2RM2001818 NT2RM2001902
NT2RM2001939 NT2RM2001941 NT2RM4000100
NT2RM4000198 NT2RM4000284 NT2RM4000295
NT2RM4000326 NT2RM4000417 NT2RM4000444
NT2RM4000587 NT2RM4000593 NT2RM4000648
NT2RM4000761 NT2RM4000965 NT2RM4001377
NT2RM4001735 NT2RM4001843 NT2RM4002352
NT2RP1000002 NT2RP1000050 NT2RP1000181
NT2RP1000239 NT2RP1000261 NT2RP1000271
NT2RP1000300 NT2RP1000325 NT2RP1000465
NT2RP1000468 NT2RP1000551 NT2RP1000579
NT2RP1000613 NT2RP1000679 NT2RP1000740
NT2RP1000981 NT2RP1001004 NT2RP1001020
NT2RP1001031 NT2RP2000092 NT2RP2000178
NT2RP2000240 NT2RP2000394 NT2RP2000447
NT2RP2000514 NT2RP2000533 NT2RP2000610
NT2RP2000616 NT2RP2000649 NT2RP2000663
NT2RP2000694 NT2RP2000712 NT2RP2000739
NT2RP2000818 NT2RP2000903 NT2RP2001200
NT2RP2001223 NT2RP2001276 NT2RP2001388
NT2RP2001469 NT2RP2001480 NT2RP2001495
NT2RP2001514 NT2RP2001529 NT2RP2001538
NT2RP2001562 NT2RP2001662 NT2RP2001755
NT2RP2001769 NT2RP2001817 NT2RP2001878
NT2RP2001903 NT2RP2001921 NT2RP2001948
NT2RP2001956 NT2RP2002063 NT2RP2002188
NT2RP2002232 NT2RP2002304 NT2RP2002409
NT2RP2002510 NT2RP2002527 NT2RP2002533
NT2RP2002564 NT2RP2002824 NT2RP2002942
NT2RP2002974 NT2RP2002976 NT2RP2003042
NT2RP2003138 NT2RP2003179 NT2RP2003210
NT2RP2003302 NT2RP2003369 NT2RP2003390
NT2RP2003469 NT2RP2003545 NT2RP2003593
NT2RP2003655 NT2RP2003664 NT2RP2003931
NT2RP2003940 NT2RP2003950 NT2RP2004069
NT2RP2004108 NT2RP2004141 NT2RP2004205
NT2RP2004447 NT2RP2004606 NT2RP2004648
NT2RP2004670 NT2RP2004794 NT2RP2004847
NT2RP2005069 NT2RP2005163 NT2RP2005181
NT2RP2005247 NT2RP2005378 NT2RP2005391
NT2RP2005425 NT2RP2005535 NT2RP2005541
NT2RP2005597 NT2RP2005632 NT2RP2005666
NT2RP2005774 NT2RP2005878 NT2RP2005883
NT2RP2005941 NT2RP2005994 NT2RP2006004
NT2RP2006042 NT2RP2006092 NT2RP2006099
NT2RP2006134 NT2RP2006269 NT2RP2006512
NT2RP3000011 NT2RP3000022 NT2RP3000059
NT2RP3000063 NT2RP3000125 NT2RP3000148
NT2RP3000171 NT2RP3000172 NT2RP3000201
NT2RP3000232 NT2RP3000304 NT2RP3000378
NT2RP3000427 NT2RP3000436 NT2RP3000444
NT2RP3000481 NT2RP3000616 NT2RP3000645
NT2RP3000652 NT2RP3000676 NT2RP3000677
NT2RP3000721 NT2RP3000820 NT2RP3000838

NT2RP3000871 NT2RP3000907 NT2RP3000921
NT2RP3001012 NT2RP3001061 NT2RP3001159
NT2RP3001170 NT2RP3001195 NT2RP3001240
NT2RP3001271 NT2RP3001322 NT2RP3001388
NT2RP3001542 NT2RP3001560 NT2RP3001592
NT2RP3001650 NT2RP3001738 NT2RP3001754
NT2RP3001976 NT2RP3002015 NT2RP3002160
NT2RP3002286 NT2RP3002311 NT2RP3002324
NT2RP3002342 NT2RP3002353 NT2RP3002409
NT2RP3002411 NT2RP3002448 NT2RP3002571
NT2RP3002664 NT2RP3002737 NT2RP3002738
NT2RP3002790 NT2RP3002836 NT2RP3002887
NT2RP3002900 NT2RP3002958 NT2RP3002983
NT2RP3003000 NT2RP3003076 NT2RP3003354
NT2RP3003448 NT2RP3003473 NT2RP3003527
NT2RP3003532 NT2RP3003614 NT2RP3003729
NT2RP3003849 NT2RP3003874 NT2RP3003939
NT2RP3004025 NT2RP3004067 NT2RP3004075
NT2RP3004090 NT2RP3004119 NT2RP3004130
NT2RP3004133 NT2RP3004202 NT2RP3004294
NT2RP3004309 NT2RP3004345 NT2RP3004406
NT2RP3004481 NT2RP3004552 NT2RP3004557
NT2RP3004625 NT2RP3004640 NT2RP3004647
NT2RP4000108 NT2RP4000634 NT2RP4000962
NT2RP4001009 NT2RP4001467 NT2RP4001877
NT2RP4001879 NT2RP4002187 NT2RP4002451
NT2RP4002750 OVARC1000003 OVARC1000090
OVARC1000105 OVARC1000137 OVARC1000255
OVARC1000275 OVARC1000307 OVARC1000313
OVARC1000331 OVARC1000410 OVARC1000439
OVARC1000467 OVARC1000529 OVARC1000553
OVARC1000873 OVARC1000916 OVARC1000956
OVARC1000995 OVARC1001030 OVARC1001049
OVARC1001086 0VAPC1001132 OVARC1001163
OVARC1001222 OVARC1001260 OVARC1001336
OVARC1001338 OVARC1001569 OVARC1001570
OVARC1001596 OVARC1001607 OVARC1001725
OVARC1001952 OVARC1001991 OVARC1002058
OVARC1002178 PLACE1000033 PLACE1000258
PLACE1000442 PLACE1000740 PLACE1000907
PLACE1001016 PLACE1001114 PLACE1001123
PLACE1001231 PLACE1001340 PLACE1001401
PLACE1001407 PLACE1001464 PLACE1001500
PLACE1001516 PLACE1001564 PLACE1001655
PLACE1001795 PLACE1001836 PLACE1001918
PLACE1001949 PLACE1002080 PLACE1002095
PLACE1002153 PLACE1002329 PLACE1002355
PLACE1002374 PLACE1002547 PLACE1002726
PLACE1002905 PLACE1002911 PLACE1002967
PLACE1003135 PLACE1003163 PLACE1003428
PLACE1003438 PLACE1003460 PLACE1003529
PLACE1003573 PLACE1003598 PLACE1003644
PLACE1003737 PLACE1003772 PLACE1003852
PLACE1004078 PLACE1004166 PLACE1004168
PLACE1004279 PLACE1004441 PLACE1004450
PLACE1004482 PLACE1004492 PLACE1004519
PLACE1004520 PLACE1004630 PLACE1004648
PLACE1004816 PLACE1004887 PLACE1005003

PLACE1005031 PLACE1005239 PLACE1005383
PLACE1005426 PLACE1005519 PLACE1005539
PLACE1005544 PLACE1005569 PLACE1005682
PLACE1005736 PLACE1005745 PLACE1005815
PLACE1005878 PLACE1005927 PLACE1006071
PLACE1006073 PLACE1006208 PLACE1006277
PLACE1006290 PLACE1006443 PLACE1006515
PLACE1006716 PLACE1006959 PLACE1007028
PLACE1007077 PLACE1007081 PLACE1007096
PLACE1007296 PLACE1007591 PLACE1007702
PLACE1007845 PLACE1007881 PLACE1008282
PLACE1008297 PLACE1008359 PLACE1008469
PLACE1008549 PLACE1008657 PLACE1008716
PLACE1008744 PLACE1008984 PLACE1008985
PLACE1009279 PLACE1009527 PLACE1009546
PLACE1009600 PLACE1009735 PLACE1010011
PLACE1010078 PLACE1010081 PLACE1010251
PLACE1010445 PLACE1010713 PLACE1010784
PLACE1010827 PLACE1010968 PLACE1011045
PLACE1011116 PLACE1011181 PLACE1011236
PLACE1011364 PLACE1011407 PLACE1011516
PLACE1011708 PLACE1011824 PLACE1011978
PLACE2000118 PLACE3000181 PLACE3000213
PLACE4000354 SKNMC1000014 SKNMC1000082
THYRO1000061 THYRO1000196 THYRO1000400
THYRO1000580 THYRO1000584 THYRO1000678
THYRO1000776 THYRO1000795 THYRO1000846
THYRO1000866 THYRO1000956 THYRO1000964
THYRO1001063 THYRO1001071 THYRO1001102
THYRO1001113 THYRO1001128 THYRO1001205
THYRO1001242 THYRO1001266 THYRO1001456
THYRO1001457 THYRO1001471 THYRO1001478
THYRO1001529 THYRO1001593 THYRO1001608
THYRO1001641 THYRO1001700 THYRO1001702
THYRO1001770 THYRO1001803 Y79AA1000030
Y79AA1000127 Y79AA1000207 Y79AA1000270
Y79AA1000426 Y79AA1000750 Y79AA1000777
Y79AA1000876 Y79AA1000888 Y79AA1000967
Y79AA1001062 Y79AA1001090 Y79AA1001212
Y79AA1001272 Y79AA1001426 Y79AA1001523
Y79AA1001727 Y79AA1001787 Y79AA1001799
Y79AA1001803 Y79AA1001863 Y79AA1002058
Y79AA1002121 Y79AA1002129 Y79AA1002213
Y79AA1002334 Y79AA1002376 Y79AA1002378
Y79AA1002381 NT2RP2006580

[0059] Among the clones, the following 83 clones are identical to the clones selected by the score in the ATGpr and the prediction by the PSORT for the existence of a signal sequence.

HEMBA1000907 NT2RM2000410 PLACE1000740
HEMBA1002164 NT2RM2001941 PLACE1001407
HEMBA1002421 NT2RP1000050 PLACE1002080
HEMBA1003101 NT2RP2001495 PLACE1002095
HEMBA1004797 NT2RP2001948 PLACE1002374
HEMBA1006335 NT2RP2002063 PLACE1003428
HEMBA1006572 NT2RP2002304 PLACE1003460
HEMBA1006707 NT2RP2003469 PLACE1004482
HEMBA1006902 NT2RP2003593 PLACE1005383

HEMBA1007013 NT2RP2003655 PLACE1005544
HEMBB1000447 NT2RP2003664 PLACE1005569
HEMBB1000567 NT2RP2004447 PLACE1005927
HEMBB1001200 NT2RP2006042 PLACE1006277
HEMBB1002427 NT2RP2006269 PLACE1006443
MAMMA1000591 NT2RP3000481 PLACE1007096
MAMMA1000681 NT2RP3000645 PLACE1007296
MAMMA1001043 NT2RP3001012 PLACE1008469
MAMMA1001893 NT2RP3001195 PLACE1008984
MAMMA1001957 NT2RP3001560 PLACE1008985
MAMMA1002070 NT2RP3002160 PLACE1009527
MAMMA1002165 NT2RP3002836 PLACE1010251
MAMMA1002633 NT2RP3002958 PLACE1011236
NT2RP3003076 SKNMC1000014
NT2RP3003354 THYPO1000196
NT2RP3004133 THYRO1000795
NT2RP3004309 THYRO1001478
NT2RP4001879 THYRO1001702
NT2RP4002451 Y79AA1000270
OVARC1000439 Y79AA1000426
OVARC1001222 Y79AA1001803
Y79AA1001863

[0060] The 446 clones in Table 16, 17, 18, 19, and 20, and NT2RP2006580 are predicted to encode a secretory or membrane protein. Among them, 77 clones were identical to the clones selected by the score in the ATGpr and the prediction by the PSORT for the existence of a signal sequence (overlapping with any of the 254 clones listed in Table 7-15). Besides, many clones were turned out to be identical to the clones selected as a protein associated with a glycoprotein. Also, there were clones identical to those selected as a protein associated with a disease.

[0061] The 243 clones in Table 21 are predicted to encode a glycoprotein. Among them, 53 clones were identical to those selected by the score in the ATGpr and the prediction by the PSORT for the existence of a signal sequence. And, many clones were turned out to be identical to the clones selected as a secretory or membrane protein. Moreover, there were clones identical to those selected as a protein associated with a disease.

[0062] The 51 clones in Table 22 are predicted to encode a protein associated to signal transduction.

[0063] The 130 clones in Table 23 are predicted to encode a protein associated to transcription.

[0064] The 17 clones in Table 24 are predicted to encode a protein associated with diseases.

[0065] In these clones, 532 clones have the maximal ATGpr1 score of 0.5 or higher (Table 25). 60 clones have the maximal ATGpr1 score of 0.3 or higher and less than 0.5 (Table 26 and NT2RP2006580). And 67 clones were with the maximal ATGpr1score of 0 or higher and less than 0.3 (Table 27).

[0066] 532 clones shown in Table 25, each having the maximal score in the ATGpr1 0.5 or higher, are very likely to be full-length and encode a secretory or membrane protein, or proteins associated to signal transduction, glycoprotein, transcription, or diseases. 59 clones in Table 26 and NT2RP2006580, which have the maximal score in the ATGpr1 0.3 or higher and less than 0.5, are likely to be full-length and encode a secretory or membrane protein, or proteins associated to signal transduction, glycoprotein, transcription, or diseases. 67 clones in Table 27, having the maximal score in the ATGpr1 0 or higher and less than 0.3, are still likely to be full-length and encode a secretory or membrane protein, or proteins associated to signal transduction, glycoprotein, transcription, or diseases.

[0067] This is the method for selecting the cDNA clones predicted to encode secretory and/or transmembrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, or disease-associated proteins on the basis of the partial sequences (5' sequences).

[0068] The polynucleotide of the present invention encodes an amino acid sequence of a functional protein such as a secretory or membrane protein, or a protein associated to signal transduction, glycoprotein, transcription, or diseases. Since the protein has the complete amino acid sequence, it is possible to analyze its biological activity by expressing the protein as a recombinant protein using an appropriate expression system, or by raising and using an antibody which specifically recognizes it.

[0069] It is possible to analyze the biological activity of a secretory protein or a membrane protein, or proteins associated to signal transduction, glycoprotein, or transcription, based on the methods in "Gene Transcription" (Hames B. D., and Higgins S.J. edit, (1993)), "Glycobiology" (Fukuda M., and Kobata A. edit, (1993)), "Growth Factors" (McKay I., and Leigh I. edit, (1993)), "Extracellular Matrix" (Haralson M.A., and Hassell J.R. edit, (1995), "Transcription Factors" (Latchman D.S. edit, (1993)), "Signal Transduction" (Milligans G. edit, (1992)), featured in "The Practical Approach

Series" (IRL PRESS), or "Signal Transduction Protocols" (Kendall D.A., and Hill S.J. edit, (1995), "Glycoprotein Analysis in Biomedicine" (Hounsell E.F. edit, (1993)), featured in "Method in Molecular Biology" (Humana Press).

[0070] As to a protein associated with a disease, it is possible to perform a functional analysis as described above, but also possible to analyze correlation between the expression or the activity of the protein and a certain disease by using a specific antibody that recognizes the protein. Alternatively, it is possible to utilize the database Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is a database of human genes and diseases, to analyze the protein. New information is constantly being deposited in the OMIM database. Therefore, it is possible for one skilled in the art to find a new relationship between a particular disease and a gene of the present invention in the updated database.

[0071] Proteins associated with diseases are useful in drug development as they can be utilized as a diagnostic marker, a drug that regulates the level of their expression and activities, or a target of gene therapy. Also, as for a secretory protein, membrane protein, or proteins associated with signal transduction, glycoprotein, or transcription, search of the OMIM with the keywords mentioned below revealed that the proteins are associated with many diseases. Also, relationship between a proteins associated to signal transduction or transcription and diseases is reported in "Transcription Factor Research-1999" (Fujii, Tamura, Morohashi, Kageyama, and Satake edit, (1999) Jikken-Igaku Zoukan, Vol.17, No.3), and "Gene Medicine" ((1999) Vol.3, No.2). Thus, not only a protein associated with diseases, but also a secretory protein, membrane protein, or protein associated with signal transduction, glycoprotein, or transcription is involved in diseases, suggesting these proteins also are very important as a target in medical industry.

[0072] Keywords used in the search of the OMIM

(1) secretion protein
(2) membrane protein
(3) channel
(4) extracellular matrix
(5) receptor
(6) glycoprotein
(7) protein kinase
(8) calmodulin kinase
(9) transcription factor

[0073] Shown in the search result are only the accession numbers in the OMIM. Using the number, data showing the relationship between a disease and a gene or protein can be seen. The OMIM data has been renewed everyday.

1) Secretion protein
268 entries found, searching for "secretion protein"
104760, 176860, 160900, 107400, 118910, 139320, 603850, 147572, 176880, 600946, 603215, 157147, 600174, 151675, 170280, 179512, 179513, 138120, 179509, 246700, 179510, 600626, 179511, 600998, 109270, 601489, 154545, 179490, 185860, 603216, 122559, 601746, 147290, 602672, 146770, 603062, 179508, 131230, 601591, 602421, 139250, 167805, 167770, 600041, 600564, 118825, 601146, 300090, 600753, 601652, 600759, 600768, 602434, 182590, 603166, 308230, 602534, 603489, 107470, 150390, 104610, 173120, 158106, 143890, 306900, 308700, 134797, 137350, 227500, 176300, 107730, 600760, 138079, 120180, 120160, 120150, 124092, 138160, 101000, 227600, 600509, 601199, 142410, 104311, 193400, 201910, 107300, 122560, 272800, 217000, 590050, 147670, 133170, 176730, 300300, 134370, 274600, 120140, 162151, 158070,
152790, 120120, 106100, 300200, 192340, 190160, 138040, 147470, 147620, 173350, 147380, 152200, 152760, 157145, 153450, 264080, 113811, 600937, 600840, 188545, 202110, 600514, 186590, 603372, 136435, 137241, 252800, 214500, 207750, 138850, 139191, 142640, 138130, 189907, 603692, 600633, 603355, 107270, 600377, 147892, 232200, 600281, 232800, 602358, 137035, 601771, 601769, 253200, 601933, 118444, 600270, 120700, 600945, 603732, 147660, 600761, 172400, 600823, 600877, 130080, 171060, 107740, 307800, 602843, 130660, 152780, 124020, 601124, 601340, 601604, 601610, 171050, 312060, 232700, 300159, 142703, 600734, 125255, 168450, 123812, 188540, 147940, 188450, 600839, 182452, 188400, 182280, 176760, 263200, 600264, 188826, 252650, 601185, 162641, 137216, 601398, 601538, 118888, 118445, 601745,
190180, 601922, 182098, 602008, 147440, 602384, 600031, 109160, 602663, 151670, 602682, 602730, 602779, 146880, 603061, 142704, 603140, 106150, 600732, 153620, 603318, 139392, 600042, 102200, 603493, 182100, 264300, 603795, 184600

2) Membrane protein
1017 entries found, searching for "membrane protein"
130500, 305360, 153330, 173610, 170995, 109270, 170993, 309060, 120920, 602333, 133740, 133710, 602690,

133730, 159430, 600897, 133090, 601178, 602413, 602003, 109280, 603237, 602173, 107776, 602334, 125305, 602335, 182879, 154045, 309845, 600594, 603718, 603241, 603214, 603657, 603177, 600182, 601476, 602879, 136950, 600723, 601114, 185880, 185881, 300096, 602257, 160900, 177070, 603062, 603344, 602977, 310200, 600959, 300100, 186945, 600039, 600267, 128240, 182900, 601097, 136430, 600946, 602534, 601047, 143450, 603141, 603700, 600579, 256540, 159440, 602414, 600403, 602048, 188860, 137290, 158343, 184756, 602910, 603179, 600279, 108733, 107770, 173335, 602625, 154050, 219800, 603850, 601028, 600447, 104225, 186946, 601767, 603143, 121015, 603215, 227400, 603735, 600179, 602421, 180721, 176801, 176860, 600753, 603142, 176790, 600266, 601239, 115501, 143890, 121014, 121011, 125950, 603534, 304040, 601134, 600754, 601510, 601595, 190315, 300172, 602216, 602261, 602262, 602461, 131560, 179514, 179512, 176981, 142461, 139310, 312080, 176640, 128239, 185470, 310300, 601403, 601757, 273800, 151460, 176943, 104311, 168468, 120130, 602887, 600164, 601531, 601832, 104775, 600040, 603583, 176894, 602631, 166945, 182180, 120620, 141180, 601014, 139150, 182860, 177061, 600174, 180069, 191275, 104760, 601693, 300017, 603518, 601009, 134651, 601107, 103868, 600168, 136425, 603531, 603291, 600917, 603216, 102720, 300118, 179590, 135630, 602285, 107450, 602296, 303630, 176878, 120090, 600322, 138160, 601212, 603293, 131230, 112205, 600763, 600718, 300187, 170715, 601966, 300051, 602474, 120070, 600691, 600855, 182309, 602101, 602857, 194355, 162230, 600874, 113730, 155550, 602701, 306400, 601789, 231200, 107271, 175100, 182870, 305100, 301000, 601313, 157147, 147670, 139200, 603593, 157655, 600934, 155970, 602049, 155960, 155760, 118990, 135620, 308230, 602694, 162060, 300023, 160993, 153619, 153432, 120131, 603823, 603167, 601023, 600816, 165040, 601681, 166490, 300112, 120190, 300145, 163970, 600772, 602926, 602933, 602202, 400015, 151510, 600759, 602672, 602654, 603821, 116952, 151430, 602632, 155975, 602217, 150370, 600752, 601179, 600932, 603048, 603234, 601805, 603822, 603869, 601717, 601181, 313440, 139130, 107777, 109190, 603452, 191163, 191164, 602370, 176877, 103195, 600523, 191328, 601275, 204200, 602426, 603820, 600551, 600695, 600552, 600553, 602306, 601523, 602507, 602299, 600583, 114070, 600632, 603498, 185430, 600587, 235200, 173470, 603199, 601633, 602500, 208900, 180297, 156225, 516020, 190195, 141900, 102680, 193300, 101000, 193400, 300011, 107400, 257220, 107741, 180380, 203200, 111700, 600024, 304800, 600065, 110750, 179605, 113705, 601638, 222900, 120120, 602509, 602469, 600930, 601383, 176261, 602574, 602997, 311770, 131550, 603616, 308700, 603372, 256100, 224100, 276903, 305900, 516000, 131195, 314555, 601567, 603866, 306900, 103390, 186720, 173850, 601050, 602505, 186590, 246530, 602689, 194380, 300041, 162643, 152790, 120150, 600682, 600106, 272750, 188040, 602382, 601497, 113811, 182138, 212138, 601309, 109690, 114760, 176805, 601253, 123900, 602581, 189980, 191190, 110700, 600163, 137167, 600580, 601610, 190000, 123825, 603491, 600135, 186591, 173910, 138140, 107266, 120950, 601081, 603690, 244400, 312700, 171060, 601199, 601758, 170500, 277900, 601997, 314850, 601880, 603009, 120220, 603126, 164920, 602934, 164730, 163890, 603434, 107269, 602909, 600877, 256550, 164761, 602872, 120110, 126150, 158070, 266200, 223360, 250800, 269920, 252650, 603355, 154582, 138190, 300035, 602640, 227650, 158120, 153700, 182380, 155740, 204500, 603401, 601975, 300135, 136350, 602924, 300167, 185050, 176100, 300189, 151525, 300200, 165180, 230800, 602158, 602676, 603411, 193245, 120325, 601848, 192500, 603102, 147795, 245900, 137060, 147557, 120650, 602377, 307800, 120930, 308100, 142800, 191092, 232300, 173510, 602225, 180470, 190930, 186357, 134638, 600544, 601373, 600509, 600359, 603784, 600395, 600653, 603754, 601597, 601066, 600185, 601295, 600978, 205400, 603274, 600418, 600839, 516050, 601691, 601007, 600650, 600308, 603261, 601193, 600004, 600017, 516040, 253800, 276901, 600019, 257200, 108780, 300037, 300104, 300126, 255125, 203300, 300191, 426000, 302060, 304700, 201475, 252010, 193210, 311030, 306250, 248600, 191740, 108360, 131244, 600423, 232200, 191305, 231680, 103320, 190180, 600493, 111200, 226200, 312600, 600170, 111680, 186910, 203100, 600536, 600238, 186830, 186760, 186745, 186711, 106180, 111203, 103180, 182530, 182160, 600644, 307030, 192321, 600667, 125647, 179080, 114207, 114860, 176000, 116930, 600748, 173515, 173325, 600377, 171760, 171050, 118425, 170260, 191315, 600798, 600821, 600823, 600444, 600840, 159465, 600857, 158380, 600867, 154360, 152427, 150330, 110900, 147840, 147360, 147280, 146880, 312610, 120940, 142871, 142790, 600937, 142600, 134390, 111250, 600979, 600997, 142460, 186845, 134635, 601017, 139191, 139090, 138850, 601040, 138720, 122561, 131100, 123610, 217070, 100500, 603377, 602354, 603302, 603207, 603086, 602188, 602095, 603867, 603842, 603798, 602602, 601194, 602607, 603713, 603681, 601252, 603648, 603646, 603644, 601282, 601284, 603667, 603712, 603594, 601872, 603425, 601843, 603263, 603208, 601411, 603201, 603189, 601463, 603164, 603152, 603087, 602874, 601492, 602893, 602057, 602859, 602746, 603879, 603510, 602458, 603380, 601581, 603765, 603283, 601599, 601733, 601852, 602316, 601615, 601617, 602184, 602894, 603005, 603030, 603861, 602835, 602136, 600153, 600074, 600046, 600023, 601625, 516006, 600018, 600016, 516002, 601590, 313475, 313470, 600244, 600528, 601611, 600282, 600327, 601568, 600368, 601730, 601535, 601745, 601929, 300169, 300150, 300132, 601533, 600385, 600464, 600424, 600429, 601756, 601488, 516005, 251100, 516004, 600918, 516003, 602192, 516001, 240500, 600465, 602241, 602243, 230200, 601485, 601478, 601416, 602297, 601459, 601839, 602314,

193065, 193001, 191306, 600504, 601020, 191191, 602372, 190181, 600534, 188380, 186854, 186360, 600530, 185250, 182331, 600535, 182305, 601296, 600582, 600732, 600734, 600742, 600782, 176802, 176266, 600769, 601883, 600864, 601901, 176260, 173490, 600910, 601905, 171890, 600916, 601987, 602679, 162651, 161555, 160994, 602714, 602715, 602724, 602736, 300007, 602783, 275630, 602836, 270200, 602871, 159460, 602876, 154540, 153900, 602890, 601153, 602190, 602905, 153634, 153337, 602914,
152310, 151690, 151625, 602935, 602974, 150325, 602992, 150320, 250790, 603006, 603007, 603008, 150292, 233690, 603046, 150210, 603061, 147940, 603063, 221770, 223100, 603097, 147880, 603118, 147730, 146928, 146630, 142622, 603149, 603150, 603151, 600923, 138981, 138590, 138330, 216950, 603192, 138297, 603202, 601002, 602343, 138230, 136131, 603217, 603220, 134660, 131390, 131235, 603242, 603243, 130130, 602345, 126455, 601123, 126064, 125240, 602359, 603312, 602380, 603318, 123890, 123836, 603356, 603361, 603366, 123830, 179610, 188060, 123620, 120980, 186355, 118510, 114835, 114217, 113810, 603499, 182310, 111740, 109610, 603548, 603564, 108740, 603598, 603613, 107273, 603626, 602518, 179410, 603647, 602515, 603652, 106195, 602573, 178990, 105210, 104615, 167055, 603717, 104614, 603728,
104210, 603749, 603750, 103850, 602608, 603787, 603788, 603796, 173445, 103220, 102910, 102681, 102670, 102642, 603833, 173391, 102576, 102575, 171833, 102573, 101800, 603875, 601108

3) Channel

272 entries found, searching for "channel"

176266, 600724, 170500, 182390, 123825, 114208, 114205, 601784, 114206, 600937, 114204, 603415, 600053, 114209, 114207, 600760, 118425, 601011, 192500, 176261, 600761, 176260, 600359, 600228, 600877, 602235, 300008, 182389, 182391, 601328, 601534, 600504, 602323, 601958, 602780, 602781, 601327, 601012, 600734, 603208, 182392, 603220, 603219, 603888, 600054, 602232, 601745, 603537, 602604, 603796, 302910, 602866, 601013, 602905, 602906, 600163, 152427, 180901, 600702, 600308, 602754, 107776, 602024, 314555, 601949, 600235, 602023, 176263, 600681, 176265, 193245, 603305, 176258, 602983, 601219, 601141, 176267, 602343, 602726, 138253, 176262, 600003, 600397, 602872, 138249, 600843, 600935, 600580, 600845, 602158, 602106, 176264, 300110, 176257, 602717, 603493, 176268, 600932, 602727, 138254,
603652, 300138, 602420, 600570, 600150, 603583, 602345, 603749, 601142, 176256, 600846, 138252, 602982, 603787, 602836, 603788, 602566, 603651, 602421, 100690, 107777, 100725, 100710, 600509, 603061, 154275, 304040, 154276, 180902, 121014, 602368, 139311, 601383, 108745, 601313, 601042, 600131, 186360, 600109, 600229, 600170, 603319, 601485, 118503, 180903, 602076, 124030, 601059, 601212, 601218, 147450, 600855, 600919, 601154, 601157, 171060, 600968, 182139, 131230, 121015, 600421, 113730, 249210, 310500, 600637, 125950, 118800, 156490, 602974, 104610, 121011, 602522, 118504, 300041, 160900, 601382, 602103, 600465, 602014, 600442, 601109, 602481, 277900, 254210, 138247, 164920, 170280, 171050, 128100, 173910, 600884, 123885, 602887, 600232, 180297, 137192, 600304, 138251, 603053, 300103,
603152, 603199, 118511, 118508, 138079, 600983, 182307, 603324, 305990, 603418, 114080, 232200, 600046, 600040, 602403, 603750, 603785, 104210, 600019, 600300, 182860, 603852, 603853, 603855, 516060

4) Extracellular matrix

167 entries found, searching for "extracellular matrix"

603479, 602201, 601418, 601548, 154870, 115437, 602285, 602262, 602261, 134797, 600754, 120361, 116935, 602263, 603320, 601807, 603321, 185250, 185261, 253700, 128239, 120324, 193300, 276901, 308700, 600514, 600261, 602109, 120140, 120150, 147557, 193400, 600536, 188826, 120180, 118661, 120320, 152200, 135821, 112260, 230740, 602090, 155760, 192975, 190182, 602108, 601463, 186745, 600900, 600985, 600758, 602369, 179590, 601211, 600065, 602178, 600262, 182888, 182889, 151510, 182120, 150325, 190181, 150370, 186355, 193065, 165070, 154705, 147559, 146650, 146640, 153619, 175100, 187380, 231050, 188060, 135820, 156790, 130660, 301870, 128240, 600076, 600119, 193210, 600215, 600245, 121010, 150240, 600309, 600491, 222600, 120328, 600564, 600596, 600616, 600700, 600742, 120325, 138297, 600930,
156225, 601028, 601050, 601105, 253800, 601284, 601313, 120280, 310200, 601492, 120250, 601587, 601636, 601652, 601692, 601728, 120220, 601915, 602048, 155120, 310300, 120210, 120165, 120120, 118940, 116930, 602264, 116806, 602366, 120470, 602415, 602428, 602453, 602505, 602574, 603005, 603196, 603221, 603319, 107269, 216550, 103320, 603489, 603551, 603767, 603799, 603842

5) Receptor (including membrane proteins, and also including transcription factors, since nuclear proteins were not excluded in the search)

1606 entries found, searching for "receptor"

600408, 176943, 107770, 601531, 143890, 313700, 162643, 202200, 147670, 191306, 182131, 192321, 138249, 190120, 600264, 162321, 603613, 603614, 602164, 138251, 182134, 138040, 152790, 602393, 133430, 601769, 304800, 147280, 168468, 147730, 155555, 191190, 109760, 122561, 136537, 602034, 147138, 187930, 312861,

107450, 138981, 182135, 603612, 191191, 600933, 601267, 600168, 120650, 182133, 601919, 108962, 162323, 102576, 600022, 603366, 600052, 136430, 601835, 600825, 600979, 102981, 192974, 602779, 601828, 603499, 601972, 191315, 602601, 603611, 602943, 601300, 191316, 108960, 601299, 147810, 602909, 601834, 108961, 602392, 602910, 603372, 106165, 601199, 180901, 131244, 107470, 136435, 146740, 164920, 139191, 138971, 109690, 100690, 138850, 118504, 147781, 146928, 601373, 126449,
104225, 100725, 164342, 104220, 118503, 136538, 137241, 601663, 601805, 306250, 600377, 600337, 600509, 600983, 126110, 118507, 602548, 162010, 601268, 147671, 601284, 113503, 109190, 603826, 154540, 147569, 600956, 138245, 139139, 155541, 137192, 118445, 104250, 300119, 118511, 601159, 100710, 305660, 104210, 114610, 138253, 146929, 602778, 135630, 147140, 146790, 147045, 601998, 158378, 131243, 600041, 118508, 137142, 113995, 138247, 182137, 147811, 182132, 138248, 600414, 600563, 137160, 138032, 601496, 138252, 138254, 601600, 173800, 146760, 179590, 180903, 109635, 300038, 138244, 182139, 600849, 600644, 601296, 602282, 179611, 143090, 100710, 601076, 600380, 170998, 600845, 118505, 118510, 190160, 104260, 137164, 137140, 600456, 147880, 137190, 601156, 601956, 100730, 601194, 602717,
173880, 600042, 180902, 300093, 602423, 602469, 603028, 601437, 146933, 179610, 173510, 600843, 305915, 137143, 603361, 603031, 137141, 136539, 162332, 118509, 155540, 600233, 601109, 601743, 600409, 147139, 131235, 603506, 603455, 151445, 602408, 601681, 603540, 602454, 602490, 600214, 600798, 600232, 602729, 600730, 601122, 120577, 160994, 603248, 602621, 601305, 176946, 118502, 176888, 602167, 138246, 158050, 601470, 603453, 603065, 137163, 137166, 600846, 118495, 138243, 192975, 138060, 602757, 191311, 603652, 120340, 600315, 136425, 118493, 600731, 601502, 601503, 601751, 603651, 602345, 118496, 601598, 602343, 118494, 186880, 134934, 601007, 600946, 186930, 186970, 133171, 308380, 120620, 126452, 190010, 126450, 186810, 180220, 173410, 188070, 131550, 109691, 147679, 180240, 173490,
300034, 264080, 114131, 146661, 147370, 147545, 136352, 190182, 186780, 126453, 110700, 147851, 308385, 126451, 128239, 600018, 601487, 601040, 305990, 601604, 190181, 188545, 162641, 600445, 231200, 136350, 601586, 164770, 600073, 602376, 138491, 118946, 176761, 176806, 601770, 180245, 164870, 602691, 600939, 109610, 192977, 159530, 602997, 164860, 300007, 146710, 601757, 150370, 118444, 600239, 138033, 601167, 108360, 162642, 173850, 603881, 180246, 193210, 173470, 601469, 134935, 182452, 138492, 135620, 601523, 601790, 600221, 109630, 602451, 147265, 602626, 602001, 602069, 601642, 600848, 102776, 180190, 182098, 176886, 602250, 182454, 600222, 600821, 180247, 602730, 134637, 167055, 165196, 165195, 173391, 601426, 600527, 600167, 153618, 601330, 601970, 600785, 600004, 601043, 109135,
109636, 601613, 600804, 601529, 102581, 600936, 126150, 182451, 300107, 190151, 602746, 165070, 170650, 600421, 100997, 602648, 603243, 300035, 305670, 182455, 162651, 109535, 601320, 120920, 603411, 603691, 601535, 102775, 601166, 180381, 176804, 602188, 600051, 601993, 601773, 603755, 600241, 601050, 603659, 600253, 300130, 137026, 602368, 154570, 176945, 602005, 120980, 602583, 102777, 600524, 602848, 173393, 601711, 104221, 176884, 600441, 108361, 600665, 600446, 600799, 600742, 104219, 603819, 600867, 602351, 601978, 600578, 602566, 600551, 601898, 151443, 602642, 300182, 191164, 602356, 603071, 602190, 601522, 182889, 142703, 601576, 100735, 176882, 602969, 182453, 601895, 602886, 602927, 602697, 601070, 120830, 601108, 176891, 176802, 600024, 600552, 601908, 176981, 603510, 151460,
602237, 602545, 162341, 603748, 161565, 600894, 186711, 137161, 601839, 601592, 603507, 602885, 430000, 104222, 601116, 602643, 601896, 601404, 601381, 600180, 600870, 123889, 600206, 600242, 602992, 601380, 602950, 602174, 603159, 602042, 602297, 602836, 602355, 602304, 603822, 147267, 603030, 603821, 602043, 603820, 603317, 601965, 601524, 601974, 603823, 602728, 601741, 137570, 603500, 602592, 153622, 601204, 186990, 601115, 600283, 182180, 600600, 600066, 600282, 176944, 600926, 600895, 300188, 602657, 602756, 600925, 182888, 603808, 603029, 602702, 602464, 603751, 425000, 601910, 151020, 600553, 603195, 602646, 601909, 603692, 136950, 600543, 164320, 300086, 602933, 602993, 137162, 603281, 153243, 161555, 600011, 600144, 600869, 600493, 602346, 600342, 602336, 113955, 602893, 601577,
603749, 602892, 603810, 602853, 600579, 601044, 603809, 186690, 600752, 603304, 600240, 603232, 600868, 602894, 602337, 603143, 109545, 602891, 602890, 602716, 603142, 602510, 603144, 603141, 300090, 602550, 603145, 107741, 107730, 164761, 208900, 107269, 114208, 235200, 158120, 147440, 300200, 161561, 186830, 151520, 131240, 139250, 601667, 153240, 218030, 147680, 186740, 600044, 107940, 153390, 102582, 600978, 601218, 142409, 601156, 601884, 601789, 125950, 171833, 602221, 139320, 147760, 190000, 184757, 601512, 165180, 166490, 168470, 601366, 176000, 191160, 102578, 103320, 112260, 192240, 109091, 603233, 134370, 254210, 173610, 125480, 600957, 118945, 120470, 136351, 600725, 176797, 602887, 173511, 123910, 601459, 252500, 104615, 601528, 600345, 601890, 151390, 602170, 186790, 186960,
600542, 186973, 600423, 600058, 176730, 186945, 104760, 601309, 601500, 300091, 113705, 214500, 602731, 600726, 176885, 164875, 139330, 104640, 147840, 600065, 131242, 164160, 600565, 601211, 151530, 603599, 180860, 190040, 147720, 222100, 223900, 600555, 600994, 186770, 120420, 602004, 601099, 603776, 601212, 132890, 600007, 158105, 603886, 603884, 176830, 162200, 602458, 601603, 107910, 193400, 133100, 160900, 114855, 601498, 601511, 116831, 131390, 107773, 137800, 155750, 147795, 264600, 114207, 244400, 187040,

126455, 164040, 147683, 263200, 188230, 184756, 147574, 179615, 176960, 176947, 147561, 131320, 107265, 147470, 264700, 173335, 124010, 147050, 132810, 230350, 276000, 114130, 155730, 134638, 254150, 122560, 186940, 208150, 188040, 188400, 100600, 601564, 603875, 603849, 601497, 603254, 603180, 602952, 602775, 602584, 602570, 601045, 600632, 602559, 601883, 600618, 601848, 601766, 601753, 600554, 600937, 600694, 311360, 302910, 600173, 300139, 300065, 274000, 305100, 300116, 300022, 163800, 187410, 187020, 603818, 105850, 107941, 307800, 601897, 212895, 603598, 603584, 603583, 603454, 603412, 601872, 114204, 266300, 114841, 116897, 152690, 603261, 603130, 603109, 603061, 603055, 603043, 601771, 154275, 600910, 187011, 188060, 600039, 600464, 186355, 121360, 122559, 123000, 253800, 602901, 125255, 131100, 600837, 602772, 600835, 131530, 602695, 137580, 602623, 139130, 249210, 142408, 602457, 600179, 142445, 154276, 245480, 142800, 600998, 602354, 601698, 602272, 601053, 602265, 231550, 229300, 147780, 601985, 147796, 226200, 600276, 147830, 150200, 601937, 189906, 601922, 600341, 100650, 601662, 189965, 159440, 190020, 601054, 600764, 600410, 153440, 205400, 601055, 203800, 600576, 600749, 190090, 601767, 600475, 190080, 154550, 184745, 601721, 601712, 600594, 600739, 600738, 180069, 601020, 601679, 162662, 601266, 601676, 601203, 172400, 601463, 600685, 601599, 164009, 600611, 601570, 600626, 600201, 600514, 191100, 195002, 600567, 600633, 191030, 190700, 600014, 303700, 308210, 308230, 191170, 269700, 191092, 192130, 600319, 238600, 195000, 600125, 600577, 261680, 600566, 266100, 309900, 266600, 306900, 600536, 194070, 201910, 188860, 188595, 257220, 600038, 202110, 261000, 600363, 600850, 306100, 602229, 603883, 102645, 186921, 186910, 603785, 186852, 104311, 107266, 107270, 603746, 603732, 109270, 602060, 602041, 148180, 151385, 151625, 123830, 182530, 123842, 124030, 134660, 153370, 134850, 601023, 182280, 134797, 182125, 134390, 601047, 135820, 601804, 153420, 601801, 139312, 139392, 181031, 601622, 180700, 147570, 603157, 162150, 601589, 121013, 151440, 602919, 151510, 123810, 123890, 131210, 179730, 602663, 179020, 602630, 601231, 601252, 137295, 138190, 138550, 277700, 601295, 139311, 153455, 176311, 176310, 601313, 133170, 141800, 142995, 602358, 143100, 145505, 300079, 168461, 145981, 158070, 106700, 107400, 107720, 601485, 103950, 108330, 165360, 300300, 156490, 603492, 602018, 118485, 164951, 164730, 164720, 147620, 603406, 164343, 119530, 161560, 142910, 602414, 601933, 120290, 164013, 164012, 600667, 601534, 601513, 601520, 164015, 164340, 173515, 164975, 302020, 160782, 601501, 165230, 302060, 165120, 601492, 601483, 167040, 167415, 600714, 192968, 600696, 601458, 601447, 173325, 168820, 176820, 601413, 190198, 600489, 173445, 601754, 600481, 300155, 600453, 154230, 173430, 154030, 173360, 181590, 176876, 176970, 178600, 164005, 182160, 274500, 179616, 275120, 151990, 300147, 601863, 211750, 275355, 151675, 190170, 179838, 600750, 180200, 180231, 151430, 600753, 601582, 150240, 601584, 601153, 224500, 601154, 601969, 180440, 600596, 600281, 600262, 227400, 601997, 147684, 147678, 600761, 147581, 602014, 602024, 147573, 601150, 159555, 147559, 600945, 191163, 602065, 147558, 601641, 147450, 602096, 602113, 600583, 602154, 600556, 159350, 147245, 186855, 192020, 191510, 146631, 146630, 180950, 601693, 146255, 602260, 238300, 600231, 602293, 194540, 602299, 145680, 602311, 145260, 600230, 602350, 239100, 600508, 143055, 601723, 143010, 155960, 601377, 602382, 275350, 600220, 602396, 304050, 600424, 602421, 142461, 602430, 602431, 142460, 246530, 273300, 249100, 602461, 602465, 141850, 601788, 602498, 140210, 181460, 600422, 300127, 600164, 600765, 602582, 138800, 300101, 138720, 138420, 602609, 600157, 138079, 138030, 600156, 601017, 137240, 602671, 602680, 602682, 136530, 182090, 600807, 601826, 602724, 153245, 182331, 210250, 600151, 602738, 131340, 131241, 300008, 131195, 600119, 602809, 602839, 602840, 128240, 126850, 126065, 252650, 253200, 188380, 600810, 600396, 123841, 182810, 123835, 600053, 217030, 602921, 602931, 602932, 601900, 600050, 185430, 185520, 121800, 254770, 259700, 222300, 120940, 120700, 120436, 120360, 603033, 600295, 603035, 262600, 603046, 600009, 263400, 120150, 263520, 603126, 590085, 185605, 118960, 118940, 118455, 603149, 603177, 300019, 603181, 118425, 603207, 426000, 116955, 116940, 116930, 300088, 603264, 603272, 603274, 116899, 603302, 313650, 266265, 603331, 114835, 603356, 114830, 312760, 603378, 602061, 310400, 603414, 603437, 113730, 310200, 113710, 147557, 113000, 112205, 111400, 111100, 110750, 603518, 603526, 602136, 603576, 309845, 603594, 308310, 108728, 108355, 600250, 307200, 603628, 107777, 602165, 603653, 600899, 107273, 107271, 603695, 603705, 603717, 186590, 186720, 186760, 186820, 187700, 600916, 147183, 105590, 104610, 146770, 306400, 602227, 103390, 103280, 103070, 102670, 301000, 603851, 600874, 600871, 102200, 158380, 603889

6) Glycoprotein

438 entries found, searching for "glycoprotein"

231200, 273800, 138700, 138600, 173510, 173515, 192974, 109770, 138610, 603578, 195002, 182889, 601275, 602977, 300051, 173470, 171050, 138680, 142640, 194460, 176390, 138720, 600119, 185430, 138670, 180297, 171060, 600073, 173335, 128239, 118850, 602616, 110700, 164345, 159465, 159460, 191845, 173511, 600564, 159440, 256550, 153310, 168810, 600738, 151460, 138470, 190197, 603586, 601325, 601193, 162820, 158120, 155970, 190920, 603201, 603594, 601411, 155735, 186730, 601028, 158030, 176391, 115501, 137290, 601103,

600315, 176870, 601525, 601418, 137061, 137207, 137060, 176397, 176393, 176394, 182888, 160995, 176398, 600718, 176396, 176392, 176399, 176401, 176395, 125645, 601774, 104175, 195000, 601785, 193400, 600065, 111200, 253700, 152200, 154550, 310200, 188230, 256540, 120980, 130660, 107269, 158070, 156790, 131550, 135630, 138297, 155760, 231050, 603381, 143890, 176801, 118860, 103600, 193210, 186820, 114890, 188060, 118910, 107271, 153340, 313470, 600074, 603062, 109270, 602724, 603356, 120324, 192340, 266265, 110900, 306400, 601327, 118457, 151250, 136836, 253000, 104640, 190010, 190000, 135620, 135600, 601852, 134797, 134370, 111250, 156225, 600596, 187430, 164870, 151510, 186720, 601962, 600900, 151530, 180990, 180290, 182120, 603759, 179605, 158381, 158373, 158343, 155740, 153420, 151675, 142800, 176300, 153240, 140100, 134820, 134660, 134390, 125240, 120520, 112205, 111740, 106100, 104225, 103000, 139090, 176860, 102720, 176895, 180621, 602421, 602257, 252600, 252650, 180620, 227600, 228960, 208900, 182145, 208400, 602643, 602593, 602461, 602171, 182900, 601269, 600270, 600033, 602894, 247100, 186910, 600239, 230500, 217800, 600867, 253220, 601581, 305600, 162060, 158378, 188450, 186880, 186990, 188040, 154582, 164022, 188540, 153634, 189965, 193190, 165095, 165220, 158375, 152790, 158374, 151627, 182205, 155750, 191316, 151523, 151020, 165330, 166490, 192225, 224050, 224100, 185490, 192240, 173445, 167770, 185050, 153619, 230800, 147740, 147730, 147670, 153618, 236200, 193300, 249000, 176385, 153440, 147557, 152310, 253270, 184900, 182331, 146760, 146661, 272300, 272800, 142930, 169615, 171640, 182520, 182310, 300027, 147780, 305370, 151525, 142858, 142840, 308230, 308385, 309060, 142445, 142290, 216950, 139130, 600026, 600044, 600046, 138971, 138960, 138140, 600133, 600182, 600215, 173350, 173360, 135820, 600403, 600410, 600491, 134934, 147563, 600535, 133700, 600587, 133170, 131390, 600616, 600713, 131195, 600722, 130160, 600742, 600751, 600764, 600769, 600798, 180540, 600978, 129010, 601040, 601050, 125505, 125490, 124010, 601194, 601211, 601253, 147380, 120930, 601313, 120830, 120620, 601365, 601368, 120220, 601456, 601484, 117700, 147045, 601652, 274500, 116930, 116880, 601788, 116805, 114250, 113810, 601880, 601914, 601932, 111700, 602046, 602053, 602108, 602243, 176820, 178630, 178640, 111680, 300017, 109535, 142860, 602692, 109530, 602746, 308840, 107740, 107400, 603104, 603125, 603126, 603130, 107273, 603197, 107266, 603241, 603243, 104614, 312080, 104610, 603492, 103390, 102670, 102480, 100735, 603665, 603756, 100730, 603777

7) Protein kinase (a member of signal transduction)
729 entries found, searching for "protein kinase"
600289, 160900, 601032, 176948, 600899, 176947, 176894, 601939, 602980, 601314, 601955, 601335, 600447, 602130, 603606, 601158, 602006, 602549, 602678, 176872, 603014, 602520, 186945, 601254, 602315, 601263, 177061, 176873, 600497, 603607, 602449, 602740, 602898, 602741, 300083, 602899, 114080, 603412, 601184, 602739, 176910, 600050, 176949, 602741, 602743, 600341, 601951, 601212, 600038, 156490, 600855, 600758, 603455, 156491, 603424, 300075, 180381, 151510, 600168, 600085, 601890, 602896, 602123, 600221, 602904, 602687, 176945, 602897, 600222, 602098, 601685, 176944, 109635, 601795, 601679, 603722, 602521, 601436, 191164, 602004, 176942, 601684, 300101, 601299, 601434, 602615, 601435, 176960, 153390, 603166, 179090, 300300, 176871, 602216, 176912, 176893, 603453, 300185, 177060, 176943, 176981, 603441, 176970, 116899, 603442, 311550, 603495, 169190, 600448, 602399, 176946, 176977, 188830, 602350, 601591, 601782, 137026, 400008, 300094, 600058, 600831, 176892, 601639, 602919, 176911, 176975, 300172, 603072, 600583, 177015, 176982, 176980, 603248, 176941, 602757, 600870, 603440, 148750, 601959, 600869, 602448, 600408, 306000, 266200, 602539, 602425, 600160, 310200, 208900, 600997, 186973, 305360, 179611, 307030, 603262, 601050, 602758, 147795, 311800, 600664, 600441, 603251, 600527, 313650, 123831, 191315, 602958, 123832, 602989, 602614, 123828, 136350, 601284, 602940, 601329, 600173, 171834, 124095, 603464, 603584, 116953, 300035, 600600, 109135, 601232, 601988, 603850, 603384, 603184, 602990, 125855, 601047, 603460, 603258, 602748, 603723, 164870, 603368, 139310, 601818, 602913, 603005, 602221, 173570, 147670, 602610, 600524, 113508, 251170, 142370, 142408, 191306, 147796, 118423, 600286, 601074, 600765, 600922, 179610, 602747, 601953, 601132, 600136, 601288, 601289, 602297, 191316, 601535, 602925, 125450, 602839, 602168, 602461, 105590, 114085, 600714, 154235, 603261, 109270, 191305, 602625, 602366, 602749, 600927, 300134, 603496, 136352, 176790, 600073, 601523, 115441, 191170, 114210, 116900, 188250, 102576, 603764, 603497, 603304, 601934, 602255, 600004, 600526, 601589, 600856, 601269, 601465, 601207, 601935, 600863, 602394, 601983, 602048, 300200, 179050, 164761, 189980, 602626, 137025, 602694, 602731, 125305, 123810, 300139, 601792, 275350, 171833, 193525, 601540, 162200, 601826, 116898, 601108, 601528, 600954, 602609, 602838, 603167, 601522, 600505, 600431, 600267, 188555, 600140, 308240, 600137, 600011, 151410, 601530, 134934, 116952, 300142, 191311, 601603, 603889, 601728, 165160, 165070, 136351, 601836, 601839, 133090, 601595, 602745, 602516, 154950, 603601, 602052, 154045, 603583, 600695, 602933, 602756, 601014, 602474, 602887, 172270, 601366, 180220, 602189, 114105, 600963, 603369, 601296, 603289, 602265, 602337, 600066, 600456, 602387, 600917, 139270, 603271, 188345, 601231, 115440, 115442, 600778, 164920, 175100, 310300, 601767, 603168, 603140, 603113,

116940, 162060, 603048, 603275, 601146, 600434, 602336, 602310, 602308, 147522, 603311, 227645, 114110, 601114, 300022, 164785, 167414, 123280, 600007, 600560, 229300, 151430, 176740, 602426, 109636, 602775, 108355, 601999, 601524, 190151, 202500, 601592, 600723, 102750, 600753, 603618, 603814, 147521, 602514, 603015, 602525, 602524, 172471, 602647, 602590, 600864, 172470, 602538, 602527, 602526, 143890, 164730, 232300, 131550, 116951, 601713, 154550, 603434, 138160, 601702, 126335, 272800, 601497, 602038, 107940, 191190, 273800, 193300, 120150, 603068, 603259, 102582, 601099, 253700, 308000, 602338, 602689, 185605, 164040, 600119, 152690, 601496, 602188, 123900, 602860, 164960, 600618, 601045, 300189, 164860, 602505, 230800, 141850, 147545, 110300, 600051, 138600, 233700, 109700, 238600, 109690, 253800, 311770, 156225, 603719, 191030, 309000, 601893, 190030, 189972, 601247, 190120, 600179, 258501, 190040, 300121, 180380, 314850, 600438, 306400, 179715, 190450, 600636, 180901, 173335, 601290, 154500, 131195, 115460, 603078, 603775, 603760, 158900, 602354, 102680, 122560, 602382, 103320, 603597, 603510, 232600, 133170, 603353, 603345, 603318, 603309, 230400, 139250, 603296, 603272, 114240, 147557, 232400, 139259, 602122, 230200, 164014, 248600, 601703, 194364, 150000, 602102, 601683, 158070, 602170, 602007, 601306, 248610, 601387, 161770, 132800, 164760, 601902, 601253, 173470, 602930, 603691, 165360, 123835, 603544, 147265, 107777, 602377, 600605, 602869, 601121, 602388, 301300, 590060, 601059, 168461, 142600, 314555, 142410, 170290, 602498, 190090, 311030, 142409, 190181, 600966, 308100, 600936, 171900, 190182, 172405, 102600, 603754, 600281, 172430, 138249, 300039, 603154, 602642, 300041, 602659, 192240, 603473, 136537, 603134, 182280, 603084, 125660, 189990, 133430, 603755, 603302, 600737, 300144, 305400, 188545, 600652, 189940, 600633, 603009, 181031, 182160, 148500, 602384, 600650, 602190, 171150, 173490, 164765, 147780, 600910, 601272, 147880, 125255, 120090, 173390, 602668, 600483, 602995, 602996, 180860, 142445, 116949, 602681, 603027, 182125, 600327, 600799, 164757, 230450, 602730, 600782, 164880, 232700, 116935, 602303, 603203, 164710, 600244, 600206, 263200, 300034, 601487, 600980, 600956, 601985, 600884, 601956, 191041, 601568, 601586, 155960, 602288, 176761, 113900, 600581, 516050, 190070, 164940, 600544, 107941, 312861, 602373, 123836, 106165, 103850, 274270, 601922, 602355, 147420, 311010, 163800, 600536, 602018, 307200, 603619, 603652, 193001, 193245, 603729, 603752, 118888, 603796, 305600, 603852, 603853, 603886

8) Calmodulin kinase (a member of signal transduction)
35 entries found, searching for "calmodulin binding"
300172, 114180, 302020, 139312, 602584, 602293, 600310, 603379, 114106, 602350, 114105, 114213, 138249, 153430, 177061, 182520, 102680, 600489, 601478, 306000, 600490, 600922, 601302, 601568, 168890, 164795, 163730, 602698, 602699, 602987, 102681, 603384

9) Transcription factor
717 entries found, searching for "transcription factor"
305371, 189963, 164177, 600297, 600298, 163260, 189907, 173110, 600733, 189903, 189972, 600438, 600281, 189962, 157670, 602272, 600609, 189968, 189971, 189889, 107580, 189908, 601748, 601542, 601632, 600610, 189969, 600480, 601760, 176310, 603022, 600519, 601750, 123803, 600520, 600494, 164176, 602460, 603246, 113725, 107773, 189904, 602228, 147141, 132890, 189964, 164175, 142410, 313650, 164011, 164014, 164005, 601714, 600492, 164012, 601878, 600673, 600635, 191523, 602191, 600490, 602149, 189967, 140580, 164343, 603256, 600727, 600729, 600728, 140581, 600571, 601511, 102582, 189906, 600660, 124097, 314310, 600860, 600662, 184756, 600777, 600013, 600172, 600489, 601425, 600786, 600502, 602406, 600743, 189965, 603257, 602751, 602542, 603148, 603107, 603789, 602318, 156845, 123811, 600425, 600540, 600695, 601622, 147574, 601601, 602407, 602150, 601538, 600663, 603306, 165170, 187040, 602444, 189902, 189973, 600659, 600661, 601010, 600788, 602617, 601602, 602053, 601742, 300039, 602438, 602976, 600744, 602543, 602479, 600481, 600473, 603739, 600426, 603738, 189901, 603677, 600427, 603255, 600607, 600379, 189909, 601679, 600787, 602160, 601043, 601397, 601044, 600366, 300025, 602575, 602669, 601804, 601801, 176312, 176311, 600746, 602480, 602944, 600967, 600912, 306700, 306900, 193400, 601206, 480000, 191160, 601861, 164008, 600475, 600773, 600772, 600774, 142409, 156490, 600589, 601490, 151385, 600599, 184757, 602955, 234000, 603433, 603349, 603198, 602294, 600390, 603628, 147620, 600211, 601787, 601863, 147470, 603795, 603734, 152760, 104155, 128990, 601729, 600197, 147370, 173490, 603423, 600822, 188595, 603243, 600573, 601689, 142765, 603181, 600879, 603731, 600288, 602295, 121360, 164874, 300019, 162095, 602355, 603258, 126090, 159540, 300070, 600555, 600664, 601874, 153245, 191191, 601126, 601512, 146733, 131550, 142385, 601796, 603406, 602959, 601734, 601732, 139191, 139139, 600633, 138971, 600006, 603170, 601488, 147576, 147680, 601498, 602630, 602643, 603364, 600914, 154040, 602746, 128992, 143089, 160900, 600140, 134934, 133510, 176860, 190180, 601150, 601175, 170993, 601361, 122560, 602778, 308230, 602903, 309550, 601788, 602946, 159970, 124092, 180200, 173410, 602356, 603015, 600779, 603111, 187930, 602614, 600951, 603200, 602369, 164770, 147569, 603300, 603301, 159980, 134638,

603431, 147730, 603366, 603348, 600556, 602136, 164160, 310200, 152390, 601241, 116897, 137295, 600576, 194070, 601487, 600698, 164810, 601769, 141900, 602225, 275350, 131100, 179755, 600075, 162200, 165160, 116806, 600899, 123810, 133450, 216400, 278700, 190080, 164730, 191170, 193300, 600618, 600999, 601090, 106150, 601843, 133530, 110700, 602550, 138040, 133430, 300133, 163731, 602302, 126337, 309548, 180245, 126110, 602291, 109565, 107400, 314670, 601444, 143100, 104760, 106180, 601953, 600584, 125852, 602419, 600401, 142200, 107680, 167414, 600020, 188400, 208900, 175100, 602700, 601828, 139320, 602777, 600185, 602681, 603023, 314997, 602848, 600284, 102578, 114290, 165095, 137070, 602991, 602421, 600005, 602996, 314995, 152200, 151900, 112260, 129010, 600892, 273800, 167660, 602341, 490000, 136533, 400003, 601007, 602229, 603620, 602218, 602116, 602020, 142000, 601955, 126340, 120150, 193067, 182452, 142461, 194558, 180660, 600756, 160745, 107741, 106210, 157640, 186770, 146738, 603759, 213700, 147880, 152391, 277900, 151626, 107730, 600711, 600246, 107470, 600237, 223100, 107748, 600065, 600349, 426000, 194500, 154030, 227650, 600247, 314980, 109560, 305370, 600800, 301000, 277700, 600838, 312173, 600439, 600440, 191315, 601595, 190450, 190070, 190020, 162360, 131320, 133540, 600993, 601993, 159530, 601902, 602868, 181590, 601724, 602260, 601093, 187270, 164761, 602102, 603245, 136950, 106100, 601182, 167410, 601897, 602896, 170100, 602506, 104150, 176730, 601600, 187011, 102600, 180380, 162080, 603450, 142967, 602301, 126375, 603372, 603355, 164720, 603250, 167409, 167415, 602897, 601565, 185250, 182138, 601851, 600749, 601575, 194548, 154500, 601365, 194541, 601621, 601623, 601531, 600790, 194355, 123830, 123812, 154540, 601415, 143055, 601386, 194550, 186930, 131290, 601320, 601620, 601754, 601313, 184430, 182900, 182500, 600725, 147870, 154365, 116953, 601297, 601296, 601265, 600796, 120436, 601644, 601930, 601643, 230200, 601645, 601972, 600861, 602009, 601172, 601158, 601646, 180630, 600821, 118440, 601656, 601647, 150200, 601125, 601671, 141850, 116899, 600697, 109270, 202110, 150570, 601108, 191339, 601063, 109691, 180240, 203100, 151430, 179710, 111000, 176797, 238600, 104311, 240300, 125255, 600423, 158070, 602439, 600324, 112261, 243305, 602474, 174762, 600613, 602539, 138890, 138720, 114550, 173865, 602582, 602584, 173510, 600250, 602627, 173325, 602635, 246530, 172425, 600193, 602691, 600188, 170998, 152790, 168468, 256540, 225250, 600848, 143400, 168461, 262600, 168360, 601912, 602951, 600017, 230000, 266600, 602981, 272800, 109150, 102200, 603025, 603026, 603109, 167050, 603127, 603128, 165240, 230400, 313700, 164975, 164875, 602017, 115500, 235800, 164873, 602110, 164785, 164772, 312865, 603296, 600542, 164740, 602125, 309801, 602148, 300007, 306955, 603368, 116940, 602181, 603416, 126650, 163920, 300024, 603437, 602209, 603576, 603607, 305435, 600944, 180410, 303630, 159557, 301870, 132810, 100790, 603849, 603862, 603881.

[0074] There are several methods for analyzing the expression levels of genes associated with diseases. Differences in gene expression levels between diseased and normal tissues are studied by the analytical methods, for example, Northern hybridization and differential display. Other examples include a method with high-density cDNA filter, a method with DNA microarray and methods with PCR amplification (Experimental Medicine, Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional volume) DNA Microarray and Advanced PCR Methods, Muramatsu & Naba (eds.), Shujunsya). The levels of gene expression between diseased tissues and normal tissues can be studied by any of these analytical methods. When explicit difference in expression level is observed for a gene, it can be concluded that the gene is closely associated with a disease or disorder. Instead of diseased tissues, cultured cells can be used for the assessment. Similarly, when gene expression is explicitly different between normal cells and cells reproducing disease-associated specific features, it can be concluded that the gene is closely associated with a disease or disorder. When the expression levels of genes are evidently varied during major cellular events (such as differentiation and apoptosis), the genes are involved in the cellular events and accordingly are candidates for disease- and/or disorder-associated genes. Further, genes exhibiting tissue-specific expression are genes playing important parts in the tissue functions and, therefore, can be candidates for genes associated with diseases and/or disorders affecting the tissues.

[0075] For example, non-enzymic protein glycation reaction is believed to be a cause for a variety of chronic diabetic complications. Accordingly, in endothelial cells, genes, of which expression levels are elevated or decreased in a glycated protein-dependent manner, are associated with diabetic complications caused by glycated proteins (Diabetes 1996, 45 (Suppl. 3), S67-S72; Diabetes 1997, 46 (Suppl. 2), S19-S25). The onset of rheumatoid arthritis is thought to be involved in the proliferation of synovial cells covering inner surfaces of joint cavity and in inflammatory reaction resulted from the action of cytokines produced by leukocytes infiltrating into the joint synovial tissues (Rheumatism Information Center, http://www.rheuma-net.or.jp/). Recent studies have also revealed that tissue necrosis factor (TNF)-α participates in the onset (Current opinion in immunology 1959, 11, 657-662). When the expression of a gene exhibits responsiveness to the action of TNF on synovial cells, the gene is considered to be involved in rheumatoid arthritis. Many genes acting at the downstream of TNF- and IL-1. among inflammation-associated cytokines have been previously identified. The respective stimulations are transduced through independent pathways of signaling cascade. There exists another signaling cascade for both stimulations, wherein NF-κB is a common transducing molecule shared by

the two stimulations (J. Leukoc. Biol., 1994, 56(5): 542-547). It has also been revealed that many inflammation-associated genes, including IL-2, IL-6 and G-CSF, are varied in the expression levels in response to the signal through the common pathway (Trends Genet. 1999, 15(6): 229-235). It is assumed that genes of which expression levels are varied in response to the stimulation of TNF-. or IL-1. also participate in inflammation. Genes associated with neural differentiation can be candidates for causative genes for neurological diseases as well as candidates for genes usable for treating the diseases.

[0076] Clones exhibiting differences in the expression levels thereof can be selected by using gene expression analysis. The selection comprises, for example; analyzing cDNA clones by using high-density cDNA filter; and statistically treating the multiple signal values (signal values of radioisotope in the radiolabeled probes or values obtained by measuring fluorescence intensities emitted from the fluorescent labels) for the respective clones by two-sample t-test, where the signal values are determined by multiple experiments of hybridization. The clones of interest are selectable based on the statistically significant differences in the signal distribution at $p<0.05$. However, selectable clones with significant difference in the expression levels thereof may be changed depending on the partial modification of statistical treatment. For example, the clones may be selected by conducting statistical treatment with two-sample t-test at $p<0.01$; or genes exhibiting more explicit differences in the expression levels thereof can be selected by performing statistical treatment with a pre-determined cut-off value for the significant signal difference. An alternative method is that the expression levels are simply compared with each other, and then, the clones of interest are selected based on the ratio of the expression levels thereof.

[0077] Clones exhibiting differences in the expression levels can also be selected by comparing the expression levels by PCR analysis, for example, by using the method of determining the band intensities representing the amounts of PCR products with ethidium bromide staining; the method of determining the radioisotopic signal values or fluorescence intensities of the PCR products when radio-labeled or fluorescence-labeled primers; or the method of determining the values of radioisotope signals or fluorescence intensities of the probes hybridized to the PCR products when radio-labeled or fluorescence-labeled probes, respectively, are used in the hybridization. If the expression level ratios obtained in multiple PCR experiments are constantly at least 2-fold, such a clone can be judged to exhibit the difference in the expression level. When the ratios are several-fold or not less than 10-fold, the clone can be selected as a gene exhibiting the explicit difference in the expression level.

[0078] A survey of genes of which expression levels are varied specifically to the glycated protein in the endothelial cells revealed three genes with elevated expression levels, NT2RP2001538, NT2RP4001001 and Y79AA1000967. These clones are genes associated with diabetes.

[0079] A survey of genes of which expression levels are varied in response to TNF. (Tumor Necrosis Factor-alpha) in the primary cell culture of synovial tissue detected the following clones with elevated expression levels in the presence of TNF.:

BNGH41000020, HEMBA1000349, HEMBA1000634, HEMBA1000671, HEMBA1000835, HEMBA1000962, HEMBA1002178, HEMBA1002195, HEMBA1002239, HEMBA1002420, HEMBA1002524, HEMBA1002992, HEMBA1003315, HEMBA1003392, HEMBA1003487, HEMBA1003602, HEMBA1004067, HEMBA1004797, HEMBA1005337, HEMBA1005489, HEM3A1006916, HEMBB1000668, HEMBB1000905, HEMBB1001547, HEMBB1001573, HEMBB1002041, HEMBB1002663, MAMMA1000652, MAMMA1000810, MAMMA1001634, MAMMA1002091, MAMMA1002234, NT2RM2000306, NT2RM4000417, NT2RP1000002, NT2RP1000181, NT2RP1000740, NT2RP2000694, NT2RP2001921, NT2RP2002527, NT2RP2004495, NT2RP2004606, NT2RP2005163, NT2RP2005463, NT2RP2006134, NT2RP3000171, NT2RP3000652, NT2RP3001195, NT2RP3001976, NT2RP3003473, NT2RP3003874, NT2RP3004090, NT2RP3004294, NT2RP3004557, NT2RP3004647, NT2RP4000108, NT2RP4001001, NT2RP4001877, OVARC1000090, OVARC1000105, OVARC1000275, OVARC1000439, OVARC1001607, PLACE1000740, PLACE1000927, PLACE1001016, PLACE1001100, PLACE1001464, PLACE1001500, PLACE1001918, PLACE1002095, PLACE1002547, PLACE1003644, PLACE1004519, PLACE1005031, PLACE1005410, PLACE1005736, PLACE1006219, PLACE1006809, PLACE1008716, PLACE1010081, THYRO1001770, Y79AA1000127, Y79M1000207, Y79AA1000270, Y79AA1000876, Y794A1001013, Y79AA1001264, Y79AA1001272, Y79AA1001328, Y79AA1001430, Y79AA1001530, Y79AA1001799

[0080] Clones with decreased expression levels in the presence of TNF□ are NT2RM4000326, NT2RP1000300, NT2RP2000514, NT2RP2001755, NT2RP2006042, NT2RP3000481, NT2RP3002790. These clones are candidates for rheumatoid arthritis-associated genes.

[0081] A survey of genes of which expression levels are varied in response to TNF. (Tumor Necrosis Factor-alpha) or IL-1. (Interleukin-1 beta) in a human T cell strain, Jurkat cell, revealed the following clones with elevated expression levels in the presence of TNF.:

MAMMA1000141, MAMMA1000788, MAMMA1001237, MAMMA1002070,NT2RM2000582, NT2RM2002109, NT2RP1000679, NT2RP2003664, NT2RP2004108, NT2RP2005597, NT2RP3001592, NT2RP3002738, NT2RP3004133, NT2RP3004294, NT2RP3004321, NT2RP3004557, PLACE1002547, PLACE1003573,

PLACE1004305, PLACE1008744, PLACE1010011, PLACE1010713, PLACE1011181, Y79AA1000776, Y79AA1002129

[0082] The survey also revealed a clone of which expression level was decreased in the presence of TNF. The clone is PLACE1002070. The same survey further revealed the clones of which expression levels were elevated in the presence of IL-1. The clones are MAMMA1000614, MAMMA1001237, NT2RM2000514 and NT2RP3001159. These clones are genes associated with inflammation.

[0083] A survey of genes of which expression levels are varied in response to the stimulation for inducing cell differentiation (stimulation using retinoic acid (RA) or using RA/inhibitor (inhibitor for cell division)) in cultured cells of neural strain, NT2, revealed the following clones with elevated expression levels in the presence of RA:

HEMBA1000121, HEMBA1000275, HEMBA1000300, HEMBA1000634, HEMBA1000671, HEMBA1000875, HEMBA1001184, HEMBA1001390, HEMBA1001886, HEMBA1002163, HEMBA1002227, HEMBA1002420, HEMBA1002421, HEMBA1003072, HEMBA1003120, HEMBA1003294, HEMBA1003497, HEMBA1004007, HEMBA1004110, HEMBA1004391, HEMBA1004444, HEMBA1005230, HEMBA1005246, HEMBA1005267, HEMBA1005489, HEMBA1005913, HEMBA1006299, HEMBA1006357, HEMBA1006517, HEMBA1006544, HEMBA1006658, HEMBA1006749, HEMBA1007063, HEMBA1007241, HEMBB1000447, HEMBB1000542, HEMBB1000567, HEMBB1000642, HEMBB1000668, HEMBB1001026, HEMBB1001847, HEMBB1002051, HEMBB1002120, HEMBB1002228, HEMBB1002693, MAMMA1000106, MAMMA1000141, MAMMA1000473, MAMMA1000528, MAMMA1000810, MAMMA1000881, MAMMA1001634, MAMMA1001957, MAMMA1002205, MAMMA1002224, NT2RM2000423, NT2RM2000497, NT2RM2000582, NT2RM2001126, NT2RM2001902, NT2RM4000198, NT2RM4000284, NT2RM4000593, NT2RM4001321, NT2RP1000002, NT2RP1000050, NT2RP1000181, NT2RP1000261, NT2RP1000465, NT2RP1000468, NT2RP1000579, NT2RP1000679, NT2RP2000092, NT2RP2000479, NT2RP2000610, NT2RP2000663, NT2RP2000694, NT2RP2000903, NT2RP2001388, NT2RP2001538, NT2RP2001878, NT2RP2002015, NT2RP2002304, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002974, NT2RP2002976, NT2RP2003179, NT2RP2003302, NT2RP2003383, NT2RP2003469, NT2RP2003664, NT2RP2003940, NT2RP2004069, NT2RP2004108, NT2RP2004524, NT2RP2004556, NT2RP2004670, NT2RP2005069, NT2RP2005247, NT2RP2005425, NT2RP2005463, NT2RP2005514, NT2RP2005535, NT2RP2005541, NT2RP2005774, NT2RP2005878, NT2RP2005883, NT2RP2005887, NT2RP2006099, NT2RP2006134, NT2RP3000011, NT2RP3000125, NT2RP3000171, NT2RP3000232, NT2RP3000460, NT2RP3000481, NT2RP3000652, NT2RP3000677, NT2RP3000818, NT2RP3000820, NT2RP3001044, NT2RP3001061, NT2RP3001170, NT2RP3001240, NT2RP3001322, NT2RP3001388, NT2RP3001542, NT2RP3001592, NT2RP3001976, NT2RP3002790, NT2RP3002900, NT2RP3002983, NT2RP3003000, NT2RP3003354, NT2RP3003532, NT2RP3003729, NT2RP3003874, NT2RP3003939, NT2RP3004025, NT2RP3004083, NT2RP3004090, NT2RP3004130, NT2RP3004202, NT2RP3004294, NT2RP3004640, NT2RP4000108, NT2RP4000634, NT2RP4002451, NT2RP4002715, OVARC1000090, OVARC1000208, OVARC1000275, OVARC1000553, OVARC1000775, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000995, OVARC1001030, OVARC1001049, OVARC1001132, OVARC1001596, OVARC1002178, PLACE1000258, PLACE1000442, PLACE1000927, PLACE1000986, PLACE1001100, PLACE1001123, PLACE1001795, PLACE1002518, PLACE1002547, PLACE1002967, PLACE1003407, PLACE1003428, PLACE1003644, PLACE1003839, PLACE1004078, PLACE1004441, PLACE1004450, PLACE1005669, PLACE1005682, PLACE1005736, PLACE1005768, PLACE1005815, PLACE1006073, PLACE1006208, PLACE1007296, PLACE1007626, PLACE1008282, PLACE1008984, PLACE1008985, PLACE1010445, PLACE1011708, PLACE1011978, PLACE4000455, SKNMC1000004, THYRO1000036, THYRO1000580, THYRO1000776, THYRO1000999, THYRO1001063, THYRO1001128, THYRO1001205, THYRO1001327, THYRO1001523, THYRO1001725, THYRO1001770, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1001056, Y79AA1001062, Y79AA1001090, Y79AA1001727, Y79AA1002213, Y79AA1002381

[0084] The survey also revealed the clones of which expression levels were decreased in the presence of RA. The clones are BNGH41000020, HEMBA1005070, NT2RP2005027, NT2RP3003473 and Y79AA1002376.

[0085] The same survey further revealed the following clones with elevated expression levels in the presence of RA/inhibitor:

HEMBA1000128, HEMBA1000875, HEMBA1001390, HEMBA1002163, HEMBA1002227, HEMBA1002421, HEMBA1004391, HEMBA1004454, HEMBA1004785, HEMBA1005913, HEMBA1006171, HEMBA1006299, HEMBA1006335, HEMBA1006544, HEMBA1007241, HEMBB1000447, HEMBB1000668, MAMMA1000994, MAMMA1001344, NT2RM2000582, NT2RP1001004, NT2RP2000663, NT2RP2000694, NT2RP2000903, NT2RP2001388, NT2RP2002674, NT2RP2002974, NT2RP2003383, NT2RP2004069, NT2RP2004606, NT2RP2004837, NT2RP2005069, NT2RP2005425, NT2RP2005463, NT2RP2005541, NT2RP2005883, NT2RP2005887, NT2RP3000460, NT2RP3000838, NT2RP3001044, NT2RP3001240, NT2RP3001388,

NT2RP3002721, NT2RP3002738, NT2RP3003469, NT2RP3004083, NT2RP3004130, NT2RP3004202, NT2RP3004294, NT2RP3004640, NT2RP4000108, NT2RP4002451, NT2RP4002715, OVARC1000275, OVARC1000467, OVARC1000553, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000995, OVARC1001030, OVARC1001222, OVARC1001596, OVARC1002058, OVARC1002178, PLACE1000927, PLACE1001123, PLACE1001407, PLACE1001464, PLACE1001564, PLACE1001795, PLACE1002547, PLACE1003407, PLACE1003644, PLACE1003845, PLACE1004441, PLACE1004482, PLACE1005410, PLACE1005601, PLACE1005725, PLACE1005736, PLACE1006093, PLACE1006219, PLACE1006290, PLACE1006716, PLACE1007296, PLACE1007626, PLACE1008359, PLACE1010968, PLACE1011364, PLACE1011824, THYRO1000678, THYRO1000776, THYRO1000999, THYRO1001113, THYRO1001237, THYRO1001523, Y79AA1000226, Y79AA1000888, Y79AA1001430

[0086] The same survey further revealed the following clones with elevated expression levels in the presence of RA/inhibitor:

HEMBA1000349, HEMBA1001297, HEMBA1001878, HEMBA1005070, HEMBA1006482, HEMBB1001959, NT2RM2001939, NT2RP1000981, NT2RP2001469, NT2RP3003473, OVARC1001132, PLACE1001655, Y79AA1000127, Y79AA1002381. These clones are associated with neural differentiation and, therefore, are candidates for genes associated with neurological diseases.

[0087] Based on the functional analyses using a secretory protein, membrane protein, or proteins associated with signal transduction, glycoprotein, transcription, or diseases, it is possible to develop a medicine.

[0088] In case of a membrane protein, it is most likely to be a protein that functions as a receptor or ligand on the cell surface. Therefore, it is possible to reveal a new relationship between a ligand and receptor by screening the membrane protein of the invention based on the binding activity with the known ligand or receptor. Screening can be performed according to the known methods.

[0089] For example, a ligand against the protein of the invention can be screened in the following manner. Namely, a ligand that binds to a specific protein can be screened by a method comprising the steps of: (a) contacting a test sample with the protein of the invention or a partial peptide thereof, or cells expressing these, and (b) selecting a test sample that binds to said protein, said partial peptide, or said cells.

[0090] On the other hand, for example, screening using cells expressing the protein of the present invention that is a receptor protein can also be performed as follows. It is possible to screen receptors that is capable of binding to a specific protein by using procedures (a) attaching the sample cells to the protein of the invention or its partial peptide, and (b) selecting cells that can bind to the said protein or its partial peptide.

[0091] In a following screening as an example, first the protein of the invention is expressed, and the recombinant protein is purified. Next, the purified protein is labeled, binding assay is performed using a various cell lines or primary cultured cells, and cells that are expressing a receptor are selected (Growth and differentiation factors and their receptors, Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjyo, Arai, Taniguchi, and Muramatsu edit, p203-236, Tokyo-Kagaku-Doujin). A protein of the invention can be labeled with RI such as ^{125}I, and enzyme (alkaline phosphatase etc.). Alternatively, a protein of the invention may be used without labeling and then detected by using a labeled antibody against the protein. The cells that are selected by the above screening methods, which express a receptor of the protein of the invention, can be used for the further screening of an agonists or antagonists of the said receptor.

[0092] Once the ligand binding to the protein of the invention, the receptor of the protein of the invention or the cells expressing the receptor are obtained by screening, it is possible to screen a compound that binds to the ligand and receptor. Also it is possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor, for example) by utilizing the binding activities.

[0093] When the protein of the invention is a receptor, the screening method comprises the steps of (a) contacting the protein of the invention or cells expressing the protein of the invention with the ligand, in the presence of a test sample, (b) detecting the binding activity between said protein or cells expressing said protein and the ligand, and (c) selecting a compound that reduces said binding activity when compared to the activity in the absence of the test sample. Furthermore, when the protein of the invention is a ligand, the screening method comprises the steps of (a) contacting the protein of the invention with its receptor or cells expressing the receptor in the presence of samples, (b) detecting the binding activity between the protein and its receptor or the cells expressing the receptor, and (c) selecting a compound that can potentially reduce the binding activity compared to the activity in the absence of the sample.

[0094] Samples to screen include cell extracts, expressed products from a gene library, synthesized low molecular compound, synthesized peptide, and natural compounds, for example, but are not construed to be listed here. A compound that is isolated by the above screening using a binding activity of the protein of the invention can also be used as a sample.

[0095] A compound isolated by the screening may be a candidate to be an agonist or an antagonist of the receptor of the protein. By utilizing an assay that monitors a change in the intracellular signaling such as phosphorylation which results from reduction of the binding between the protein and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the receptor. Also, the compound may be a candidate of a molecule that can

inhibit the interaction between the protein and its associated proteins (including a receptor) in vivo. Such compounds can be used for developing drugs for precaution or cures of a disease with which the protein is associated.

[0096] Secretory proteins may regulate cellular conditions such as growth and differentiation. It is possible to find out a novel factor that regulates cellular conditions by adding the secretory protein of the invention to a certain kind of cell, and performing a screening by utilizing the cellular changes in growth or differentiation, or activation of a particular gene.

[0097] The screening can be performed, for example, as follows. First, the protein of the invention is expressed and purified in a recombinant form. Then, the purified protein is microinjectedadded into a various kind of cell lines or primary cultured cells, and the change in the cell growth and differentiation is monitored. The induction of a particular gene that is known to be involved in a certain cellular change is detected with the amounts of mRNA and protein. Alternatively, the amount of an intracellular molecule (low molecular compounds, etc.) that is changed by the function of a gene product (protein) that is known to be functioning in a certain cellular change is used for the detection.

[0098] Once the screening reveals that the protein of the invention can regulate cellular conditions or the functions, it is possible to apply the protein as a pharmaceutical and diagnostic medicine for associated diseases by itself or by altering a part of it into an appropriate composition.

[0099] As is above described for membrane proteins, the secretory protein provided by the invention may be used to explore a novel ligand-receptor interaction using a screening based on the binding activity to a known ligand or receptor. A similar method can be used to identify an agonist or antagonist. The resulting compounds obtained by the methods can be a candidate of a compound that can inhibit the interaction between the protein of the invention and an interacting molecule (including a receptor). The compounds may be able to use as a preventive, therapeutic, and diagnostic medicine for the diseases, in which the protein may play a certain role.

[0100] Proteins associated with signal transduction or transcription may be a factor that affects a certain protein or gene in response to intracellular/extracellular stimuli. It is possible to find out a novel factor that can affect a protein or gene by expressing the protein provided by the invention in a certain types of cells, and performing a screening utilizing the activation of a certain intracellular protein or gene.

[0101] The screening may be performed as follows. First, a transformed cell expressing the protein is obtained. Then, the transformed cell line and the untransformed original cell are compared for the changes in the expression of a certain gene by detecting the amount of its mRNA or protein. Alternatively, the amount of an intracellular molecule (low molecular compounds), which is changed by the function of a gene product (protein) that is known to function in a certain cellular change, may be used for the detection. Furthermore, the change of the expression of a certain gene can be detected by introducing a fusion gene that comprises a regulatory region of the gene and a marker gene (luciferase, beta-galactosidase, etc.) into a cell, expressing the protein provided by the invention into the cell, and estimating the activity of a marker gene product (protein).

[0102] If the protein or gene of the invention is associated with diseases, it is possible to screen a gene or compound that can regulate its expression and/or activity either directly or indirectly by utilizing the protein of the present invention.

[0103] For example, the protein of the invention is expressed and the recombinant protein is purified. Then, the protein and gene whose expression was affected in the presence of the protein of the invention is also purified, and the binding activity between the two proteins or genes is examined. The examination may be performed with pretreatment with a compound that is candidate of an inhibitor. In an alternative method, a transcription regulatory region locating in the 5'-upstream of the gene encoding the protein of the invention that is capable of regulating the expression of other genes is obtained, and fused with a marker gene. The fusion is introduced into a cell, and the cell is added with compounds to explore a regulatory factor of the expression of the said gene.

[0104] The compound obtained by the screening can be used for developing pharmaceutical and diagnostic medicines for the diseases with which the protein of the present invention is associated. Similarly, if the regulatory factor obtained by the screening is a protein, the protein itself can be used as a pharmaceutical, and if there is a compound that affects the original expression level and/or activity of the protein, it also can be used for the same purpose.

[0105] If the protein of the invention has an enzymatic activity, regardless of whether it is a secretory protein, membrane protein, or proteins associated with signal transduction, glycoprotein, transcription, or diseases, a screening may be performed by adding a compound to the protein of the invention under the suitable condition and monitoring the change of the compound. The enzymatic activity may also be utilized to screen for a compound that can inhibit the activity of the protein.

[0106] In a screening given as an example, the protein of the invention is expressed and the recombinant protein is purified. Then, compounds are contacted with the purified protein, and the amount of the compound and the reaction products is examined. Alternatively, compounds that are candidates of an inhibitor are pretreated, then a compound (substrate) that can react with the purified protein is added, and the amount of the substrate and the reaction products is examined.

[0107] The compounds obtained in the screening may be used as a medicine for diseases with which the protein of the invention is associated. Also they can be applied for tests that examine whether the protein of the invention functions

normally *in vivo*.

[0108] Whether the secretory or membrane protein of the present invention is a novel protein associated with diseases or not is determined in another method than described above, by obtaining a specific antibody against the protein of the invention, and examining the relationship between the expression or activity of the protein and a certain disease. In an alternative way, it may be analyzed referred to the methods in "Molecular Diagnosis of Genetic Diseases" (Elles R. edit, (1996) in the series of "Method in Molecular Biology" (Humana Press).

[0109] Disease-associated proteins are a target of the above described screenings and very useful for developing a drug that is capable of regulating the expression and activity of the protein. Also, they are useful in medicinal industry as a diagnostic marker of the related disease and as a target for gene therapy.

[0110] Compounds isolated as mentioned above can be administered patients as it is, or after formulated into a pharmaceutical composition according to the known methods. For example, a pharmaceutically acceptable carrier or vehicle, specifically sterilized water, saline, plant oil, emulsifier, or suspending agent can be mixed with the compounds appropriately. The pharmaceutical compositions can be administered to patients by a method known to those skilled in the art, such as intraarterial intravenous, or subcutaneous injections. The dosage may vary depending on the weight or age of a patient, or the method of administration, but those skilled in the art can choose an appropriate dosage properly. If the compound is encoded by DNA, the DNA can be cloned into a vector for gene therapy, and used for gene therapy. The dosage of the DNA and the method of its administration may vary depending on the weight or age of a patient, or the symptoms, but those skilled in the art can choose properly.

[0111] The protein encoded by the polynucleotide of the invention can be prepared as a recombinant protein or as a natural protein. For example, the recombinant protein can be prepared by inserting the polynucleotide encoding the protein of the invention into a vector, introducing the vector into an appropriate host cell and purifying the protein expressed within the transformed host cell, as described below. In contrast, the natural protein can be prepared, for example, by utilizing an affinity column to which an antibody against the protein of the invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 16.1-16.19) is attached. The antibody used for the affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, in vitro translation (See, for example, "On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) Nucleic Acids Res. 17: 3129-3144) may be used for preparing the protein of the invention.

[0112] Proteins functionally equivalent to the proteins of the present invention can be prepared based on the activities, which were clarified in the above-mentioned manner, of the proteins of the present invention. Using the biological activity possessed by the protein of the invention as an index, it is possible to verify whether or not a particular protein is functionally equivalent to the protein of the invention by examining whether or not the protein has said activity.

[0113] Proteins functionally equivalent to the proteins of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into an amino acid sequence of a protein (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5). Besides, such proteins can be generated by spontaneous mutations. The present invention comprises the proteins having one or more amino acid substitutions, deletions, insertions and/or additions in the amino acid sequences of the proteins of the present invention (Table 370), as far as the proteins have the equivalent functions to those of the proteins identified in the present Examples described later.

[0114] There are no limitations in the number and sites of amino acid mutations, as far as the proteins maintain the functions thereof. The number of mutations is typically 30% or less, or 20% or less, or 10% or less, preferably within 5% or less, or 3% or less of the total amino acids, more preferably within 2% or less or 1% or less of the total amino acids. From the viewpoint of maintaining the protein function, it is preferable that a substituted amino has a similar property to that of the original amino acid. For example, Ala, Val, Leu, Ile, Pro, Met, Phe and Trp are assumed to have similar properties to one another because they are all classified into a group of non-polar amino acids. Similarly, substitution can be performed among non-charged amino acid such as Gly, Ser, Thr, Cys, Tyr, Asn, and Gln, acidic amino acids such as Asp and Glu, and basic amino acids such as Lys, Arg, and His.

[0115] In addition, proteins functionally equivalent to the proteins of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using the hybridization technique (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)), those skilled in the art can usually isolate a DNA highly homologous to the DNA encoding the protein identified in the present Example based on the identified nucleotide sequence (Table 370) or a portion thereof and obtain the functionally equivalent protein from the isolated DNA. The present invention includes proteins encoded by the DNAs hybridizing with the DNAs encoding the proteins identified in the present Example, as far as the proteins are functionally equivalent to the proteins identified in the present Example. Organisms from which the functionally equivalent proteins are isolated are illustrated by vertebrates such as human, mouse, rat, rabbit, pig and bovine, but are not limited to these animals.

[0116] Washing conditions of hybridization for the isolation of DNAs encoding the functionally equivalent proteins are usually "1×SSC, 0.1% SDS, 37°; more stringent conditions are "0.5xSSC, 0.1% SDS, 42.°; and still more stringent conditions are "0.1 x SSC, 0.1% SDS, 65.°. Alternatively, the following conditions can be given as hybridization con-

ditions of the present invention. Namely, conditions in which the hybridization is done at "6xSSC, 40% Formamide, 25.", and the washing at "1xSSC, 55." can be given. More preferable conditions are those in which the hybridization is done at "6xSSC, 40% Formamide, 37.", and the washing at "0.2xSSC, 55.". Even more preferable are those in which the hybridization is done at "6xSSC, 50% Formamide, 37.", and the washing at "0.1xSSC, 62.". The more stringent the conditions of hybridization are, the more frequently the DNAs highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5xSSC, 0.1% SDS, 42.", or alternatively, hybridization conditions of "6xSSC, 40% Formamide, 37.", and the washing at "0.2xSSC, 55.". However, the above-mentioned combinations of SSC, SDS and temperature conditions are indicated just as examples. Those skilled in the art can select the hybridization conditions with similar stringency to those mentioned above by properly combining the above-mentioned or other factors (for example, probe concentration, probe length and duration of hybridization reaction) that determines the stringency of hybridization.

[0117] The amino acid sequences of proteins isolated by using the hybridization techniques usually exhibit high homology to those of the proteins of the present invention, which are shown in Table 370. The present invention encompasses a polynucleotide comprising a nucleotide sequence that has a high identity to the nucleotide sequence of claim 8 (a). Furthermore, the present invention encompasses a peptide, or protein comprising an amino acid sequence that has a high identity to the amino acid sequence encoded by the polynucleotide of claim 8 (b). The term "high identity" indicates sequence identity of at least 40% or more; preferably 60% or more; and more preferably 70% or more. Alternatively, more preferable is identity of 90% or more, or 93% or more, or 95% or more, furthermore, 97% or more, or 99% or more. The identity can be determined by using the BLAST search algorithm.

[0118] With the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)) using primers designed based on the nucleotide sequence (Table 370) or a portion thereof identified in the present Example, it is possible to isolate a DNA fragment highly homologous to the nucleotide sequence or a portion thereof and to obtain functionally equivalent protein to a particular protein identified in the present Example based on the isolated DNA fragment.

[0119] The "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sei. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sei. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol.215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, score = 50, wordlength = 3. When gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res.25:3389-3402,1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) are used. See http://www.ncbi.nlm.nih.gov.

[0120] The present invention also includes a partial peptide of the proteins of the invention. The partial peptide comprises a protein generated as a result that a signal peptide has been removed from a secretory protein. If the protein of the present invention has an activity as a receptor or a ligand, the partial peptide may function as a competitive inhibitor of the protein and may bind to the receptor (or ligand). In addition, the present invention comprises an antigen peptide for raising antibodies. For the peptides to be specific for the protein of the invention, the peptides comprise at least 7 amino acids, preferably 8 amino acids or more, more preferably 9 amino acids or more, and even more preferably 10 amino acids or more. The peptide can be used for preparing antibodies against the protein of the invention, or competitive inhibitors of them, and also screening for a receptor that binds to the protein of the invention. The partial peptides of the invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or digesting the protein of the invention with an appropriate peptidase.

[0121] The present invention also relates to a vector into which the DNA of the invention is inserted. The vector of the invention is not limited as long as it contains the inserted DNA stably. For example, if E. coli is used as a host, vectors such as pBluescript vector (Stratagene) are preferable as a cloning vector. To produce the protein of the invention, expression vectors are especially useful. Any expression vector can be used as far as it is capable of expressing the protein in vitro, in E. coli, in cultured cells, or in vivo. For example, pBEST vector (Promega) is preferable for in vitro expression, pET vector (Invitrogen) for E. coli, pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell. Biol. (1988) 8: 466-472) for in vivo expression. To insert the DNA of the invention, ligation utilizing restriction sites can be performed according to the standard method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 11.4-11.11).

[0122] The present invention also relates to a transformant carrying the vector of the invention. Any cell can be used as a host into which the vector of the invention is inserted, and various kinds of host cells can be used depending on the purposes. For strong expression of the protein in eukaryotic cells, COS cells or CHO cells can be used, for example.

[0123] Introduction of the vector into host cells can be performed, for example, by calcium phosphate precipitation method, electroporation method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 9.1-9.9), lipofectamine method (GIBCO-BRL), or microinjection method, etc.

[0124] The primer of the present invention can be used for synthesizing full-length cDNA, and also for the detection and/or diagnosis of the abnormality of the protein of the invention encoded by the full-length cDNA. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using the primer of the invention, DNA encoding the protein of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization since the transcription start site within the genomic sequence can be easily specified based on the 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of the abnormality of the sequence by RFLP analysis, SSCP, or direct sequencing.

[0125] Furthermore, the "polynucleotide having a length of at least 15 nucleotides, comprising a nucleotide sequence that is complementary to a polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs in Table 370, or its complementary strand" includes an antisense polynucleotide for suppressing the expression of the protein of the invention. To exert the antisense effect, the antisense polynucleotide has a length of at least 15 bp or more, for example, 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and has a length of usually 3000 bp or less and preferably 2000 bp or less. The antisense DNA can be used in the gene therapy of the diseases that are caused by the abnormality of the protein of the invention (abnormal function or abnormal expression). Said antisense DNA can be prepared, for example, by the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) Nucleic Acids Res. 16: 3209-3221) based on the nucleotide sequence of the DNA encoding the protein (for example, the DNA set forth in any one of SEQ ID NOs in Table 370).

[0126] The polynucleotide or antisense DNA of the present invention can be used in gene therapy, for example, by administrating it into a patient by the in vivo or ex vivo method with virus vectors such as retrovirus vectors, adenovirus vectors, and adeno-associated virus vectors, or non-virus vectors such as liposome.

[0127] The present invention also relates to antibodies that bind to the protein of the invention. There are no limitations in the form of the antibodies of the invention. They include polyclonal antibodies, monoclonal antibodies, or their portions that can bind to the protein of the invention. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies are also included.

[0128] The polyclonal antibody of the invention can be obtained according to the standard method by synthesizing an oligopeptide corresponding to the amino acid sequence and immunizing rabbits with the peptide (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 11.12-11.13). The monoclonal antibody of the invention can be obtained according to the standard method by purifying the protein expressed in E. coli, immunizing mice with the protein, and producing a hybridoma cell by fusing the spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 11.4-11.11).

[0129] The antibody binding to the protein of the present invention can be used for purification of the protein of the invention, and also for detection and/or diagnosis of the abnormalities of the expression and structure of the protein. Specifically, proteins can be extracted, for example, from tissues, blood, or cells, and the protein of the invention is detected by Western blotting, immunoprecipitation, or ELISA, etc. for the above purpose.

[0130] Furthermore, the antibody binding to the protein of the present invention can be utilized for treating the diseases that associates with the protein of the invention. If the antibodies are used for treating patients, human antibodies or humanized antibodies are preferable in terms of their low antigenicity. The human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of human ("Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez M.J. et al. (1997) Nat. Genet. 15: 146-156). The humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

[0131] The present invention further relates to databases comprising at least a sequence of polynucleotide and/or protein, or a medium recorded in such databases, selected from the sequence data of the nucleotide and/or the amino acids indicated in Table 370. The term "database" means a set of accumulated information as machine-searchable and readable information of nucleotide sequence. The databases of the present invention comprise at least one of the novel nucleotide sequences of polynucleotide provided by the present invention. The databases of the present invention can consist of only the sequence data of the polynucleotide provided by the present invention or can comprise other information on nucleotide sequences of known full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only the information on the nucleotide sequences but also the information on the gene functions revealed by the present invention. Additional information such as names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

[0132] The database of the present invention is useful for gaining complete gene sequence information from partial sequence information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing the information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method, the information on the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue.

[0133] The sequence information of the full-length cDNAs constituting the database of the present invention contains not only the information on the complete sequences but also extra information on expression frequency of the genes

as well as homology of the genes to known genes and known proteins. Thus the extra information facilitates rapid functional analyses of partial gene fragments. Further, the information on human genes is accumulated in the database of the present invention, and therefore, the database is useful for isolating a human homologue of a gene originating from other species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

[0134] At present, information on a wide variety of gene fragments can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene fragment corresponds to an already-known gene, the full-length sequence is easily obtained by comparing the partial sequence with the information in known databases. However, when there exists no information corresponding to the partial sequence of interest in the known databases, cDNA cloning should be carried out for the full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using the partial sequence information as an initial clue. If the full-length of the gene is not available, the amino acid sequence of the protein encoded by the gene remains unidentified. Thus the database of the present invention can contribute to the identification of full-length cDNAs corresponding to gene fragments, which cannot be revealed by using databases of known genes.

[0135] The invention is illustrated more specifically with reference to the following examples, but is not to be construed as being limited thereto.

EXAMPLE 1

Construction of a cDNA library by the oligo-capping method.

[0136] The NT-2 neuron progenitor cells (Stratagene), a teratocarcinoma cell line from human embryo testis, which can differentiate into neurons by treatment with retinoic acid were used. The NT-2 cells were cultured according to the manufacturer's instructions as follows.

(1) NT-2 cells were cultured without induction by retinoic acid treatment ((NT2RM1, NT2RM2, NT2RM4)).
(2) After cultured, NT-2 cells were induced by adding retinoic acid, and then were cultured for 48 hours (NT2RP1).
(3) After cultured, NT-2 cells were induced by adding retinoic acid, and then were cultured for 2 weeks (NT2RP2, NT2RP3, NT2RP4).

[0137] Also, the human brain neuroglioma cell line H4 (ATCC HTG-148) (BNGH41), human neuroblastoma cell line SK-N-MC (ATCC HTB-10) (SKNMC1), and human retinoblastoma cell line Y79 (ATCC HTB-18) (Y79AA1) were cultured according to the culture conditions described in the ATCC catalogue. The cells were harvested separately, and mRNA was extracted from each cell by the method described in the literature (Molecular Cloning 2nd edition. Sambrook J., Fritsch, E.F., and Maniatis T. (1989) Cold Spring Harbor Laboratory Press). Furthermore, poly(A)$^+$RNA was purified from the mRNA using oligo-dT cellulose.

[0138] Similarly, human placenta (PLACE1, PLACE2, PLACE3), human ovary cancer tissue (OVARC1), tissues from human embryo at 10 weeks, which is enriched with head (HEMBA1), or body (HEMBB1), human mammary gland (MAMMA1), human thyroid gland (THYRO1) were used to extract mRNA by the method described in the literature (Molecular Cloning 2nd edition. Sambrook J., Fritsch, E.F., and Maniatis T. (1989) Cold Spring Harbor Laboratory Press). Furthermore, poly(A)$^+$RNA was purified from the mRNA using oligo-dT cellulose.

[0139] Each poly(A)$^+$RNA was used to construct a cDNA library by the oligo-capping method (Maruyama M. and Sugano S. (1994) Gene 138: 171-174). Using the Oligo-cap linker (SEQ ID NO: 2541) and the Oligo-dT primer (SEQ ID NO: 2542), bacterial alkaline phosphatase (BAP) treatment, tobacco acid phosphatase (TAP) treatment, RNA ligation, the first strand cDNA synthesis, and removal of RNA were performed as described in the reference (Suzuki and Kanno (1996) Protein Nucleic acid and Enzyme. 41: 197-201; Suzuki Y. et al. (1997) Gene 200: 149-156). Next, 5'- and 3'-PCR primers (SEQ ID NO: 2543, and 2544, respectively) were used for performing PCR to convert the cDNA into double stranded cDNA, which was then digested with SfiI. Then, the DraIII-cleaved pUC19FL3 vector (Figure 1; for NT2RM1, and NT2RP1), or the DraIII-cleaved pME18SFL3 (Figure 1) (GenBank AB009864, expression vector; for NT2RM2, NT2RM4, NT2RP2, NT2RP3, NT2RP4, BNGH41, SKNMC1, Y79AA1, PLACE1, PLACE2, PLACE3, OVARC1, HEMBA1, HEMBB1, MAMMA1, and THYRO1) was used for cloning the cDNA in an unidirectional manner, and cDNA libraries were obtained. Then, the nucleotide sequence of the 5'- and 3'- ends of the cDNA clones was analyzed with a DNA sequencer (ABI PRISM 377, PE Biosystems) after sequencing reactions were performed with the DNA sequencing reagents (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit, or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, from by PE Biosystems) according to the instructions. The data were compiled into a database.

[0140] The full-length-enriched cDNA libraries except those for NT2RM1 and NT2RP1 were constructed using eukaryotic expression vector pME18SFL3. The vector contains SRα promoter and SV40 small t intron in the upstream

of the cloning site, and SV40 polyA added signal sequence site in the downstream. As the cloning site of pME18SFL3 has asymmetrical DraIII sites, and the ends of cDNA fragments contain SfiI sites complementary to the DraIII sites, the cloned cDNA fragments can be inserted into the downstream of the SRα promoter unidirectionally. Therefore, clones containing full-length cDNA can be expressed transiently by introducing the obtained plasmid directly into COS cells. Thus, the clones can be analyzed very easily in terms of the proteins that are the gene products of the clones, or in terms of the biological

[0141] Herein, the cDNA libraries and the name of each clone are related as shown in Table 2. Therein, "xxxxxx" represents the clone number of six digits. Thus, the sequences are named by the library name, the clone number plus F- for the 5'-end, or R- for the 3'-end.

Table 2

library: clone	5'-end sequence	3'-end sequence
NT2RM1:		
NT2RM1xxxxxx	F-NT2RM1xxxxxx	
NT2RP1:		
NT2RP1xxxxxx	F-NT2RP1xxxxxx	
NT2RM2:		
NT2RM2xxxxxx	F-NT2RM2xxxxxx	R-NT2RM2xxxxxx
NT2RM4:		
NT2RM4xxxxxx	F-NT2RM4xxxxxx	R-NT2RM4xxxxxx
NT2RP2:		
NT2RP2xxxxxx	F-NT2RP2xxxxxx	R-NT2RP2xxxxxx
NT2RP3:		
NT2RP3xxxxxx	F-NT2RP3xxxxxx	R-NT2RP3xxxxxx
NT2RP4:		
NT2RP4xxxxxx	F-NT2RP4xxxxxx	R-NT2RP4xxxxxx
BNGH41:		
BNGH41xxxxxx	F-BNGH41xxxxxx	R-BNGH41xxxxxx
SKNMC1:		
SKNMC1xxxxxx	F-SKNMC1xxxxxx	R-SKNMC1xxxxxx
Y79AA1:		
Y79AA1xxxxxx	F-Y79AA1xxxxxx	R-Y79AA1xxxxxx
PLACE1:		
PLACE1xxxxxx	F-PLACE1xxxxxx	R-PLACE1xxxxxx
PLACE2:		
PLACE2xxxxxx	F-PLACE2xxxxxx	R-PLACE2xxxxxx
PLACE3:		
PLACE3xxxxxx	F-PLACE3xxxxxx	R-PLACE3xxxxxx
OVARC1:		
OVARC1xxxxxx	F-OVARC1xxxxxx	R-OVARC1xxxxxx
HEMBA1:		
HEMBA1xxxxxx	F-HEMBA1xxxxxx	R-HEMBA1xxxxxx
HEMBB1:		
HEMBB1xxxxxx	F-HEMBB1xxxxxx	R-HEMBB1xxxxxx
MAMMA1:		
MAMMA1xxxxxx	F-MAMMA1xxxxxx	R-MAMMA1xxxxxx
THYRO1:		

THYRO1xxxxxx F-THYRO1xxxxxx R-THYRO1xxxxxx

EXAMPLE 2

Estimation of the fullness ratio of the 5'-ends of the clones contained in the cDNA libraries constructed by the oligo-capping method.

[0142] The fullness ratio at the 5'-end sequences of the 59,823 clones in the human cDNA libraries constructed by the oligo-capping method was determined as follows. Of all the clones whose 5'-end sequences were found in those of known human mRNA in the public database, a clone was judged to be "full-length", if it had a longer 5'-end sequence than that of the known human mRNA, or, even though the 5'-end sequence was shorter, if it contained the translation initiation codon. A clone which did not contain the translation initiation codon was judged to be "non-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and non-full-length clones)) at the 5'-end of the cDNA clones from each library was determined by comparing with the known human mRNA. As a result, the fullness ratio of the 5'-ends was 63.5%. It suggests that the human cDNA clones obtained by the described method have complete 5'-ends with high probability.

EXAMPLE 3

Assessment of the fullness ratio of the 5'-end of the cDNA by the ATGpr and the ESTiMateFL.

[0143] The ATGpr, developed by Salamov A.A., Nishikawa T., and Swindells M.B. in the Helix Research Institute, is a program for prediction of the translation start codon based on the characteristics of the sequences in the vicinity of the ATG codon. The results are shown with expectations that an ATG is a true start codon (0.05-0.94). When this program is applied to general cDNAs without considering whether or not the ATG codons in the cDNAs are the true initiation codons of the cDNAs, both the sensitivity and the specificity of the results are estimated at 66%. Here, the sensitivity means the ratio of the number of codons judged to be initiation codons by the program to the total number of true initiation codons, and the specificity means the ratio of the number of true initiation codons to the number of codons judged to be initiation codons by the program. In contrast, when the program was applied to the 5'-end sequences of the clones from the cDNA library that was obtained by the oligo-capping method and that had 65% fullness ratio, the sensitivity and specificity of evaluation of a full-length clone (clone containing the N-terminal end of ORF) were improved to 82-83% by selecting only clones having the ATGpr1 score 0.6 or higher.

[0144] Furthermore, the program was used to assess the fullness of 18,959 clones in the human cDNA libraries obtained here, which have 5'-ends matched to a known human mRNA. Briefly, the maximal ATGpr1 score of the clones was determined, and then their 5'-end sequence was compared with the known human mRNA to estimate whether the clone is full-length or not. The result was summarized in Table 3. Based on the knowledge that known mRNAs, in general, are highly expressed in the cell, the expression levels of genes having a low number in the EST hit, which represent mRNAs whose expression levels are relatively low were examined, and the result is shown in Table 4.

[0145] In the table, the number of full-length clones indicate that of clones containing the N-terminal end of ORF, and so does the number of non-full-length clones that of clones without the N-terminal end of ORF. The fullness ratio represents (the number of full-length clones)/(the number of full-length clones plus the number of non-full-length clones).

Table 3

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having a matched 5'-end with that of a known human mRNA.

maximal ATGpr1 score	number of (full-length clones plus non-full-length clones)	number of full-length clones	fullness ratio
>=0.70	11,193	9,346	83.5%
>=0.50	13,369	10,549	78.9%
>=0.30	15,489	11,340	73.2%

Table 3 (continued)

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having a matched 5'-end with that of a known human mRNA.

maximal ATGpr1 score	number of (full-length clones plus non-full-length clones)	number of full-length clones	fullness ratio
>=0.15	17,394	11,811	67.9%
>=0.00	18,959	12,046	63.5%

Table 4

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of the clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having 5 EST hits or less among the clones having a matched 5'-end with that of a known human mRNA.

maximal ATGpr1 score	number of (full-length clones plus non-full-length clones)	number of full-length clones	fullness ratio
>=0.70	2,801	1,934	69.0%
>=0.50	3,683	2,393	65.0%
>=0.30	4,683	2,707	57.8%
>=0.15	5,559	2,890	52.0%
>=0.00	6,113	3,013	49.8%

[0146] The ESTiMateFL, developed by Nishikawa and Ota in the Helix Research Institute, is a method for the selection of a clone with high fullness ratio by comparing with the 5'-end or 3'-end sequences of ESTs in the public database.

[0147] By the method, a cDNA clone is judged presumably not to be full-length if there exist any ESTs which have longer 5'-end or 3'-end sequences than the clone. The method is systematized for high throughput analysis. A clone is judged to be full-length if the clone has a longer 5'-end sequence than ESTs in the public database. Even if a clone has a shorter 5'-end, the clone is judged to be full-length if the difference in length is within 50 bases, and otherwise judged not to be full-length, for convenience. In case of the 5'-end sequence of the clones which matches a known mRNA, about 80% of the sequences that were judged to be full-length by comparing with ESTs was judged to be full-length by estimating the 5'-end sequence, as well; about 80% of the sequences that were judged to be not full-length by comparing with ESTs was judged to be not full-length by estimating the 5'-end sequence, as well. The accuracy of the prediction by comparing cDNA clones with ESTs is improved with increasing number of ESTs to be compared. However, when only a limited number of ESTs are available, the reliability becomes low. Thus, the method is effective in excluding clones with high probability of being non-full-length, from the cDNA clones that is synthesized by the oligo-capping method and that have the 5'-end sequences with about 60 % fullness ratio. In particular, the ESTiMateFL is efficiently used to estimate the fullness ratio at the 3'-end sequence of cDNA of a human unknown mRNA which has a significant number of ESTs in the public database.

[0148] The 18,959 clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence that matches a known human mRNA, were estimated by using the ATGpr and ESTiMateFL. Briefly, the 5'-end sequence that matches a known human mRNA of the respective clone was analyzed to obtain the maximal ATGpr1 score, and compared with the ORF of the known human mRNA that matches it to determine whether the clone is full-length or not. Then, the 5'-end sequence of the respective clone was analyzed by the ESTiMateFL to judge whether the clone is full-length or not. Specifically, the 5'-end sequences that match a known human mRNA of the 18,959 clones constructed by the oligo-capping method were compared with those of ESTs by the ESTiMateFL and the clones other than those that are not full-length were selected. Then, the selected clones were used to analyze the relationship between the ATGpr and the fullness ratio. The result was summarized in Table 5. Also, among the selected, the clones in which the number of the EST hit is not more than 5 were selected and analyzed. The result was summarized in Table 6, which represents the result of the analysis of mRNA with relatively low abundance.

[0149] In the Tables, the number of full-length clones, the number of non-full-length clones, and the fullness ratio indicate the number of the clones that contain the N-terminus of the ORF, the number of the clones that do not contain

the N-terminus of the ORF, and (the number of full-length clones)/(the number of full-length clones) plus (the number of non-full-length clones), respectively.

Table 5

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequence in the clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence that matches a known human mRNA, and also other than those being not full-length according to the comparison with ESTs.

maximal ATGpr1 score	number of (full-length clones plus non-full-length clones)	number of full-length clones	fullness ratio
>=0.70	9,068	8,349	92.1%
>=0.50	10,345	9,318	90.1%
>=0.30	11,425	9,964	87.2%
>=0.15	12,254	10,335	84.3%
>=0.00	12,785	10,484	82.0%

Table 6

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequence in the clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence that matches a known human mRNA, and also other than those being not full-length according to the comparison with ESTs, in which the number of the EST hit is not more than 5.

maximal ATGpr1 score	number of (full-length clones plus non-full-length clones)	number of full-length clones	fullness ratio
>=0.70	1,959	1,510	77.1%
>=0.50	2,469	1,821	73.8%
>=0.30	2,975	2,046	68.8%
>=0.15	3,368	2,164	64.3%
>=0.00	3,661	2,226	60.8%

[0150] According to the above results, it was found that, in case of using clones isolated from human cDNA libraries constructed by the oligo-capping method, the fullness ratio of the clones that have low score in the ATGpr can be improved by assessing their 5'-end sequence using the combination of the ATGpr and the ESTiMateFL. Therefore, the method was applied to select a cDNA clone with high fullness ratio.

EXAMPLE 4

Clustering of the 5'-end and 3'-end sequences of cDNA clones.

[0151] The 5'-end and 3'-end sequences of cDNA clones were obtained, and clustered separately. Briefly, data of the single pass sequencing of the determined 5'-end and 3'-end of cDNA clones was subjected to the BLAST search between the sequence data of all the clones synthesized in Example 1, and clones that are supposed to be originating from the same gene were clustered into a group. For the 5'-end sequence, those having the consensus sequence of 95% identity 300 base pairs or more are clustered into the same group. For the 3'-end sequence, those having the consensus sequence of 90% identity 200 base pairs or more are clustered into the same group. Among the clusters of the 5'-end and 3'-end sequences, the sequence having the longest lead was chosen as the representative sequence of the cluster (group).

EXAMPLE 5

Characterization of the representative sequences and the sequences of clones

[0152] Data of the 5'-end sequences of the representative sequences and clones was characterized by the following

methods:

(1) judging whether it is identical to the sequence of mRNA or ESTs from human by the BLAST search of the GenBank or SwissProt, and examining whether it is full-length by comparing with the sequences of known mRNA and ESTs from human.
(2) determining the ATGpr1 score using all the initiation codons contained within the 5'-end sequence by the ATGpr which predict fullness ratio.
(3) predicting the existence of the signal sequence using all the initiation codons contained within the 5'-end sequence by the PSORT which predict signal.
and,
(4) only with the 5'-end sequences of the representative sequences of the clusters, examining the keywords in the top hit data of the homology search of the SwissProt.

[0153] Data of the characterized representative sequences and clones was used for the final selection of the clones.

EXAMPLE 6

Identity to the human mRNA and human EST, and comparison of the 5'-end length.

[0154] The clones and the representative sequences of the clusters were judged to be identical to any human mRNA, if their 5'-end sequence has a region of 200 nucleotides or longer with 94% or more identity to the mRNA. The clones and the representative sequences of the clusters were judged to be identical to any human EST, if their 5'-end sequence has a region of 200 nucleotides or longer with 90% or more identity to the EST.

[0155] The clones and the representative sequences of the clusters were judged to be full-length in comparison with human mRNA, if their 5'-end sequence is longer than those of the mRNA, or it contains the translation initiation site. The clones and the representative sequences of the clusters were judged to be full-length in comparison with human EST in the database, if their 5'-end sequence is longer than those of the EST, or even though it is shorter, the difference in length between the two sequences is 50 nucleotides or less, for convenience. Otherwise, the clones and the representative sequences of the clusters were judged to be not full-length.

EXAMPLE 7

Prediction of the fullness ratio by the ATGpr.

[0156] The score in the ATGpr1 is the expectation to be full-length based on calculations, and the higher score reflects the higher fullness ratio as shown in Example 3. Further, the maximal ATGpr1 score represents the score obtained with all the initiation codons contained in the 5'-end sequence of the clones and the representative sequences, and are used for the characterization.

EXAMPLE 8

Prediction of the existence of a signal sequence by the PSORT.

[0157] Prediction of the existence of a signal sequence by the PSORT was performed on all of the amino acid sequences predicted from all the initiation codons in the 5'-end sequence of the clones and the representative sequences of the clusters. By analyzing the presence or absence of the sequence which is predicted to be a signal sequence, which is characteristics of the N-terminus of many secretory proteins, cDNA clones encoding a secretory protein or membrane protein were selected.

EXAMPLE 9

Prediction of the protein function by the BLAST search.

[0158] The 5'-end sequence of the representative sequences of the cluster was analyzed by the BLAST homology search of the SwissProt. The obtained top hit data was classified into those identical to the 5'-end representative sequence (identity was 90% or higher), those not identical to the 5'-end representative sequence (identity was 60% or lower, and compared sequence was not more than 25 nucleotides), and those similar to the 5'-end representative sequence (the rest of the data).

[0159] All the keywords in the SwissProt data corresponding to the top hit data were selected, and the 5'-end representative sequences were classified by the keywords relating with functions.
The keywords relating with a secretory protein or membrane protein are the followings:

growth factor,
cytokine,
hormone,
receptor,
G-protein coupled receptor,
ionic channel,
voltage-gated channel,
calcium channel,
extracellular matrix,
transmembrane, and
signal.

[0160] The keywords relating to glycoprotein is glycoprotein.
[0161] The keywords relating to signal transduction are the followings:

serine/threonine-protein kinase,
tyrosine-protein kinase, and
calmodulin-binding.

[0162] The keywords relating to transcription are the followings:

transcription regulation and activator,
transcription regulation and repressor, and
nuclear protein and repressor.

[0163] The keywords relating to diseases are disease mutation, and syndrome.
[0164] Many keywords overlapped in the respective group (receptor and transmembrane, for example), and some keywords overlapped in different groups (secretory or membrane, and diseases, etc.).

EXAMPLE 10

Selection of clones by characterization.

[0165] From the data obtained by the above characterization, clones encoding a novel secretory protein or membrane protein, or proteins with other predicted functions were selected by the combination of the ATGpr1 score and the prediction of the signal sequence by the PSORT, or according to the top hit data in the homology search of the SwissProt.
[0166] In selecting the clones, the 5'-end sequences that are identical to a human mRNA were ignored, whereas those that are identical to a human mRNA in part but obviously not identical in the other part were included. Because there were clones selected that are identical to a human mRNA in part but obviously not identical in the other part.
[0167] Also, if the finally selected clones were found to be not full-length compared with the sequences of human mRNA and ESTs, these clones were discarded.

EXAMPLE 11

A method for selection of clones by the combination of the ATGpr1 score and the prediction of the signal sequence by the PSORT (a method for selection of secretory proteins and membrane proteins that are novel and full-length).

[0168] The sequences of clones and the representative sequences of their clusters were used to obtain the maximal ATGpr1 score and predict the presence of the signal sequence. First, clones were selected based on the representative sequences of the clusters. The correspondence between the name and SEQ ID of the representative sequences used for selection (Table 368), and the correspondence between the name and SEQ ID of the introns (including the representative sequences of the 5'-end and 3'-end, and ESTs) used for selection of clones from the representative sequences of the groups (Table 369) were shown in the last part of the present specification. Therein, HRIFA and HRIRA indicate the representative sequence of the 5'-end group, and that of the 3'-end group, respectively.

[0169] In the clusters in which a single clone is contained (the sequence of the 5'-end clone = the representative sequence of the 5'-end), selected were the clones that were judged to be full-length in comparison with human mRNA and ESTs, having the maximal ATGpr1 score 0.5 or higher, and predicted to contain the signal sequence, in principle. However, in the following cases, a clone having a longer 5'-end was selected: the maximal ATGpr1 score was less than 0.5, the sequence of the 5'-end was not full-length, the clone was obviously shorter although the clone was not classified into the same cluster according to the BLAST search of the other clones, or the 5'-end sequence corresponding to the 3'-end of the other clones in the same cluster in which the 3'-end sequence of the clone was contained was found to be longer by assembling. Furthermore, if there were multiple full-length clones in the same cluster and it was not successful to determine by assembling which has the longer 5'-end, all the clones were selected. For assembling, the Sequencher(™) (Hitachi Soft Engineering) was used. As a result, the signal sequence predicted to be present in the representative sequence was not present in some of the selected clones. In some cases, the ATGpr1 score became smaller than 0.5 or 0.3. The fullness ratio in these clones was low, yet still it is possible that the clones are full-length. The clones in which the signal sequence predicted to be present in the representative sequence was not present after selection were likely to be without the signal sequence, but still it is possible that the clones encode a membrane protein.

[0170] In the clusters comprising multiple clones, in which the representative sequence of the 5'-end was predicted to contain the signal sequence, selected were the clones having the longest 5'-end sequence among the clones which were judged to be full-length compared with human mRNA and ESTs, having the maximal ATGpr1 score for the 5'-end sequence 0.5 or higher, and predicted to contain the signal sequence. However, in the following cases, a clone having a longer 5'-end was selected: the maximal ATGpr1 score was less than 0.5, the sequence of the 5'-end was not full-length, the clone was obviously shorter although the clone was not classified into the same cluster according to the BLAST search of the other clones, or the 5'-end sequence corresponding to the 3'-end of the other clones in the same cluster in which the 3'-end sequence of the clone was contained was found to be longer. Furthermore, if there were multiple full-length clones in the same cluster and it was not successful to determine by assembling which has the longer 5'-end, all the clones were selected. As a result, the signal sequence predicted to be present in the representative sequence was not present in some of the selected clones. In some cases, the ATGpr1 score became smaller than 0.5 or 0.3. The fullness ratio in these clones was low, yet still it is possible that the clones are full-length. The clones in which the signal sequence predicted to be present in the representative sequence was not present after selection were likely to be without the signal sequence at the 5'-end, but still it is possible that the clones encode a membrane protein.

[0171] Next, in the clusters comprising multiple clones, in which the representative sequence of the 5'-end was predicted to have no signal sequence, selected were the clones which were judged to be full-length compared with human mRNA and ESTs, having the maximal ATGpr1 score for the 5'-end sequence 0.5 or higher, and predicted to contain the signal sequence.

[0172] The number of the clones selected by the combination of the ATGpr1 score and the prediction of a signal sequence by the PSORT were 254. The number of the clones having the maximal ATGpr1 score 0.5 or higher, and predicted to contain a signal sequence were 170 (Table 7-10). Among the clones, 164 clones were found to have the representative sequence of the original cluster that fulfills the same conditions. On the other hand, 5 clones were selected from the representative sequences of the 5'-end of the clusters which was predicted to contain a signal sequence while the maximal ATGpr1 score was lower than 0.5. A clone was selected from the representative sequence of the 5'-end of the cluster which was predicted to have no signal sequence.

[0173] The clones that have the maximal ATGpr1 score 0.3 or higher and less than 0.5 and predicted to contain the signal sequence were 35 clones (Table 11), in which 8 clones were found to have the representative sequence of the original cluster that fulfills the same conditions. Twenty-seven clones were selected from the representative sequences of the clusters which have the maximal ATGpr1 score 0.5 or higher and were predicted to have no signal sequence.

[0174] The clones that have the maximal ATGpr1 score less than 0.3 and were predicted to contain a signal sequence were 41 clones (Table 12). The clones that have the maximal ATGpr1 score 0.5 or higher and were predicted to have no signal sequence were 4 clones (Table 13). The clones that have the maximal ATGpr1 score 0.3 or higher and less than 0.5 and were predicted to have no signal sequence were 2 clones (Table 14). The clones that have the maximal ATGpr1 score less than 0.3 and were predicted to contain a signal sequence were 2 clones (Table 15). The representative sequences of the original clusters of all the clones had the maximal ATGpr1 score 0.3 or higher, and were predicted to contain a signal sequence.

[0175] The fullness ratio of the clones having the maximal ATGpr1 score 0.5 or higher, 0.3 or higher, and 0 or higher is expected to be as shown in Table 3, 4, 5, and 6.

Table 7

The 170 clones in which the selected clones have the maximal ATGpr1 score 0.5 or higher, and were predicted to contain a signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	name of representative sequence	maximal ATGpr1 score	signal
HEMBA1000713	F-HEMBA1000713	0.67	Yes	HRIFA017729a	0.57	Yes
HEMBA1000962	F-HEMBA1000962	0.69	Yes	HRIFA000899a	0.69	Yes
HEMBA1001272	F-HEMBA1001272	0.94	Yes	HRIFA001179a	0.94	Yes
HEMBA1001297	F-HEMBA1001297	0.89	Yes	HRIFA001201a	0.89	Yes
HEMBA1002420	F-HEMBA1002420	0.6	Yes	HRIFA002195a	0.5	Yes
HEMBA1003101	F-HEMBA1003101	0.67	Yes	HRIFA002787a	0.94	Yes
HEMBA1003399	F-HEMBA1003399	0.94	Yes	HRIFA002985a	0.94	Yes
HEMBA1003732	F-HEMBA1003732	0.86	Yes	HRIFA003169a	0.86	Yes
HEMBA1004110	F-HEMBA1004110	0.59	Yes	HRIFA003379a	0.59	Yes
HEMBA1005430	F-HEMBA1005430	0.69	Yes	HRIFA020661a	0.69	Yes
HEMBA1006016	F-HEMBA1006016	0.6	Yes	HRIFA020466a	0.6	Yes
HEMBA1006171	F-HEMBA1006171	0.62	Yes	HRIFA021399a	0.62	Yes
HEMBA1006311	F-HEMBA1006311	0.94	Yes	HRIFA021594a	0.94	Yes
HEMBA1006335	F-HEMBA1006335	0.83	Yes	HRIFA012069a	0.94	Yes
HEMBA1006357	F-HEMBA1006357	0.67	Yes	HRIFA021448a	0.67	Yes
HEMBA1006658	F-HEMBA1006658	0.66	Yes	HRIFA021323a	0.66	Yes
HEMBA1006707	F-HEMBA1006707	0.66	Yes	HRIFA021499a	0.94	Yes
HEMBA1006902	F-HEMBA1006902	0.66	Yes	HRIFA021754a	0.94	Yes
HEMBA1006960	F-HEMBA1006960	0.94	Yes	HRIFA021886a	0.94	Yes
HEMBB1000276	F-HEMBB1000276	0.94	Yes	HRIFA029577a	0.94	Yes
HEMBB1000642	F-HEMBB1000642	0.94	Yes	HRIFA029779a	0.94	Yes
HEMBB1000905	F-HEMBB1000905	0.94	Yes	HRIFA009764a	0.91	Yes
HEMBB1001200	F-HEMBB1001200	0.83	Yes	HRIFA030839a	0.81	Yes
HEMBB1001407	F-HEMBB1001407	0.87	Yes	HRIFA030981a	0.87	Yes
HEMBB1001530	F-HEMBB1001530	0.6	Yes	HRIFA031062a	0.6	Yes
HEMBB1001547	F-HEMBB1001547	0.87	Yes	HRIFA031075a	0.87	Yes
HEMBB1001978	F-HEMBB1001978	0.7	Yes	HRIFA031350a	0.7	Yes
HEMBB1002162	F-HEMBB1002162	0.91	Yes	HRIFA031472a	0.91	Yes
HEMBB1002228	F-HEMBB1002228	0.53	Yes	HRIFA031510a	0.53	Yes
HEMBB1002245	F-HEMBB1002245	0.94	Yes	HRIFA032984a	0.94	Yes
HEMBB1002427	F-HEMBB1002427	0.57	Yes	HRIFA005760a	0.94	Yes
HEMBB1002465	F-HEMBB1002465	0.72	Yes	HRIFA031672a	0.72	Yes
HEMBB1002693	F-HEMBB1002693	0.64	Yes	HRIFA031895a	0.64	Yes
MAMMA1000046	F-MAMMA1000046	0.7	Yes	HRIFA024841a	0.7	Yes
MAMMA1000102	F-MAMMA1000102	0.79	Yes	HRIFA026151a	0.79	Yes
MAMMA1000118	F-MAMMA1000118	0.81	Yes	HRIFA026153a	0.81	Yes
MAMMA1000141	F-MAMMA1000141	0.8	Yes	HRIFA024554a	0.8	Yes
MAMMA1000449	F-MAMMA1000449	0.94	Yes	HRIFA026203a	0.94	Yes
MAMMA1000457	F-MAMMA1000457	0.78	Yes	HRIFA026210a	0.78	Yes
MAMMA1000652	F-MAMMA1000652	0.94	Yes	HRIFA026346a	0.94	Yes
MAMMA1000994	F-MAMMA1000994	0.84	Yes	HRIFA026735a	0.84	Yes
MAMMA1001141	F-MAMMA1001141	0.89	Yes	HRIFA027265a	0.89	Yes
MAMMA1001310	F-MAMMA1001310	0.74	Yes	HRIFA026899a	0.74	Yes
MAMMA1001344	F-MAMMA1001344	0.71	Yes	HRIFA026918a	0.71	Yes
MAMMA1002070	F-MAMMA1002070	0.6	Yes	HRIFA028371a	0.82	Yes
MAMMA1002087	F-MAMMA1002087	0.68	Yes	HRIFA027619a	0.68	Yes
MAMMA1002165	F-MAMMA1002165	0.57	Yes	HRIFA027673a	0.34	Yes
MAMMA1002205	F-MAMMA1002205	0.74	Yes	HRIFA027701a	0.74	Yes
MAMMA1002633	F-MAMMA1002633	0.53	Yes	HRIFA030461a	0.94	Yes
NT2RM2000241	F-NT2RM2000241	0.94	Yes	HRIFA020965a	0.94	Yes
NT2RM2000514	F-NT2RM2000514	0.51	Yes	HRIFA022106a	0.51	Yes
NT2RM2001643	F-NT2RM2001643	0.69	Yes	HRIFA028926a	0.69	Yes
NT2RM4000115	F-NT2RM4000115	0.56	Yes	HRIFA025792a	0.53	Yes
NT2RM4000997	F-NT2RM4000997	0.94	Yes	HRIFA029274a	0.94	Yes

1/4 (continued)

Table 8

The 170 clones in which the selected clones have the maximal ATGpr1 score 0.5 or higher, and were predicted to contain the signal sequence by the PSORT

name of clone	name of sequence	maximal	signal	name of representative sequence	maximal	signal
		ATGpr1 score			ATGpr1 score	
NT2RM4001321	F-NT2RM4001321	0.74	Yes	HRIFA024533a	0.74	Yes
NT2RM4001325	F-NT2RM4001325	0.94	Yes	HRIFA033349a	0.94	Yes
NT2RM4001768	F-NT2RM4001768	0.73	Yes	HRIFA013668a	0.5	Yes
NT2RP1000448	F-NT2RP1000448	0.62	Yes	HRIFA005356a	0.62	Yes
NT2RP1001583	F-NT2RP1001583	0.52	Yes	HRIFA006018a	0.62	Yes
NT2RP2001915	F-NT2RP2001915	0.94	Yes	HRIFA007541a	0.94	Yes
NT2RP2002015	F-NT2RP2002015	0.94	Yes	HRIFA007619a	0.94	Yes
NT2RP2002063	F-NT2RP2002063	0.87	Yes	HRIFA007659a	0.94	Yes
NT2RP2002304	F-NT2RP2002304	0.87	Yes	HRIFA007829a	0.94	Yes
NT2RP2002674	F-NT2RP2002674	0.8	Yes	HRIFA008099a	0.8	Yes
NT2RP2002721	F-NT2RP2002721	0.56	Yes	HRIFA008131a	0.56	Yes
NT2RP2003383	F-NT2RP2003383	0.67	Yes	HRIFA008606a	0.67	Yes
NT2RP2003593	F-NT2RP2003593	0.73	Yes	HRIFA008252a	0.94	Yes
NT2RP2003599	F-NT2RP2003599	0.58	Yes	HRIFA008753a	0.58	Yes
NT2RP2003655	F-NT2RP2003655	0.78	Yes	HRIFA008784a	0.83	Yes
NT2RP2004179	F-NT2RP2004179	0.83	Yes	HRIFA008827a	0.83	Yes
NT2RP2004495	F-NT2RP2004495	0.58	Yes	HRIFA009372a	0.58	Yes
NT2RP2004524	F-NT2RP2004524	0.73	Yes	HRIFA009392a	0.82	Yes
NT2RP2004556	F-NT2RP2004556	0.81	Yes	HRIFA009414a	0.81	Yes
NT2RP2004837	F-NT2RP2004837	0.94	Yes	HRIFA006216a	0.93	Yes
NT2RP2005027	F-NT2RP2005027	0.92	Yes	HRIFA004145a	0.93	Yes
NT2RP2005463	F-NT2RP2005463	0.93	Yes	HRIFA010004a	0.42	No
NT2RP2005514	F-NT2RP2005514	0.58	Yes	HRIFA010070a	0.58	Yes
NT2RP2005887	F-NT2RP2005887	0.94	Yes	HRIFA010322a	0.94	Yes
NT2RP2006269	F-NT2RP2006269	0.78	Yes	HRIFA025913a	0.57	Yes
NT2RP3000169	F-NT2RP3000169	0.94	Yes	HRIFA022262a	0.94	Yes
NT2RP3000460	F-NT2RP3000460	0.61	Yes	HRIFA022794a	0.61	Yes
NT2RP3000789	F-NT2RP3000789	0.62	Yes	HRIFA023605a	0.62	Yes
NT2RP3000818	F-NT2RP3000818	0.52	Yes	HRIFA023619a	0.52	Yes
NT2RP3001012	F-NT2RP3001012	0.67	Yes	HRIFA023129a	0.22	Yes
NT2RP3001044	F-NT2RP3001044	0.93	Yes	HRIFA007026a	0.73	Yes
NT2RP3001560	F-NT2RP3001560	0.58	Yes	HRIFA030599a	0.92	Yes
NT2RP3001685	F-NT2RP3001685	0.5	Yes	HRIFA023521a	0.5	Yes
NT2RP3001858	F-NT2RP3001858	0.94	Yes	HRIFA026490a	0.94	Yes
NT2RP3002160	F-NT2RP3002160	0.61	Yes	HRIFA005760a	0.94	Yes
NT2RP3002836	F-NT2RP3002836	0.68	Yes	HRIFA024392a	0.72	Yes
NT2RP3002958	F-NT2RP3002958	0.54	Yes	HRIFA017670a	0.91	Yes
NT2RP3003535	F-NT2RP3003535	0.94	Yes	HRIFA025498a	0.94	Yes
NT2RP3004000	F-NT2RP3004000	0.93	Yes	HRIFA025275a	0.93	Yes
NT2RP3004321	F-NT2RP3004321	0.81	Yes	HRIFA025786a	0.81	Yes
NT2RP3004355	F-NT2RP3004355	0.6	Yes	HRIFA025360a	0.6	Yes
NT2RP3004374	F-NT2RP3004374	0.58	Yes	HRIFA024533a	0.74	Yes
NT2RP4001001	F-NT2RP4001001	0.53	Yes	HRIFA009214a	0.5	Yes
NT2RP4002715	F-NT2RP4002715	0.94	Yes	HRIFA024921a	0.53	Yes
OVARC1000298	F-OVARC1000298	0.61	Yes	HRIFA004852a	0.59	Yes
OVARC1000775	F-OVARC1000775	0.7	Yes	HRIFA011347a	0.7	Yes
OVARC1000811	F-OVARC1000811	0.52	Yes	HRIFA000974a	0.39	Yes
OVARC1000853	F-OVARC1000853	0.94	Yes	HRIFA011403a	0.94	Yes
OVARC1001222	F-OVARC1001222	0.79	Yes	HRIFA022714a	0.67	Yes
OVARC1001807	F-OVARC1001807	0.52	Yes	HRIFA021069a	0.52	Yes
OVARC1001833	F-OVARC1001833	0.9	Yes	HRIFA021138a	0.9	Yes
PLACE1000231	F-PLACE1000231	0.52	Yes	HRIFA011802a	0.52	Yes
PLACE1000560	F-PLACE1000560	0.88	Yes	HRIFA012022a	0.88	Yes
PLACE1000740	F-PLACE1000740	0.57	Yes	HRIFA012151a	0.57	Yes

2/4 (continued)

Table 9

The 170 clones in which the selected clones have the maximal ATGpr1 score 0.5 or higher, and were predicted to contain the signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	name of representative sequence	maximal ATGpr1 score	signal
PLACE1000912	F-PLACE1000912	0.9	Yes	HRIFA012282a	0.9	Yes
PLACE1000914	F-PLACE1000914	0.94	Yes	HRIFA012283a	0.94	Yes
PLACE1000927	F-PLACE1000927	0.71	Yes	HRIFA012290a	0.71	Yes
PLACE1000986	F-PLACE1000986	0.51	Yes	HRIFA012333a	0.51	Yes
PLACE1001100	F-PLACE1001100	0.76	Yes	HRIFA012417a	0.76	Yes
PLACE1001183	F-PLACE1001183	0.69	Yes	HRIFA012480a	0.69	Yes
PLACE1001229	F-PLACE1001229	0.65	Yes	HRIFA012513a	0.65	Yes
PLACE1001407	F-PLACE1001407	0.83	Yes	HRIFA012668a	0.94	Yes
PLACE1001788	F-PLACE1001788	0.6	Yes	HRIFA012881a	0.6	Yes
PLACE1002374	F-PLACE1002374	0.88	Yes	HRIFA013265a	0.92	Yes
PLACE1002518	F-PLACE1002518	0.94	Yes	HRIFA018849a	0.78	Yes
PLACE1003839	F-PLACE1003839	0.67	Yes	HRIFA014178a	0.6	Yes
PLACE1003845	F-PLACE1003845	0.92	Yes	HRIFA019185a	0.92	Yes
PLACE1004199	F-PLACE1004199	0.94	Yes	HRIFA014417a	0.94	Yes
PLACE1004282	F-PLACE1004282	0.94	Yes	HRIFA014467a	0.94	Yes
PLACE1004305	F-PLACE1004305	0.87	Yes	HRIFA014482a	0.87	Yes
PLACE1004637	F-PLACE1004637	0.89	Yes	HRIFA014692a	0.89	Yes
PLACE1005005	F-PLACE1005005	0.55	Yes	HRIFA014953a	0.55	Yes
PLACE1005250	F-PLACE1005250	0.52	Yes	HRIFA015129a	0.52	Yes
PLACE1005410	F-PLACE1005410	0.61	Yes	HRIFA015236a	0.61	Yes
PLACE1005725	F-PLACE1005725	0.92	Yes	HRIFA015443a	0.92	Yes
PLACE1005768	F-PLACE1005768	0.62	Yes	HRIFA015471a	0.62	Yes
PLACE1005927	F-PLACE1005927	0.66	Yes	HRIFA015568a	0.94	Yes
PLACE1006079	F-PLACE1006079	0.56	Yes	HRIFA015671a	0.56	Yes
PLACE1006093	F-PLACE1006093	0.59	Yes	HRIFA015682a	0.59	Yes
PLACE1006219	F-PLACE1006219	0.94	Yes	HRIFA015764a	0.93	Yes
PLACE1006809	F-PLACE1006809	0.66	Yes	HRIFA016129a	0.66	Yes
PLACE1007040	F-PLACE1007040	0.87	Yes	HRIFA013288a	0.87	Yes
PLACE1007096	F-PLACE1007096	0.59	Yes	HRIFA012167a	0.82	Yes
PLACE1007626	F-PLACE1007626	0.67	Yes	HRIFA016623a	0.67	Yes
PLACE1007971	F-PLACE1007971	0.74	Yes	HRIFA016839a	0.74	Yes
PLACE1008985	F-PLACE1008985	0.66	Yes	HRIFA017457a	0.48	Yes
PLACE1009067	F-PLACE1009067	0.59	Yes	HRIFA017509a	0.59	Yes
PLACE1009196	F-PLACE1009196	0.73	Yes	HRIFA017594a	0.73	Yes
PLACE1009527	F-PLACE1009527	0.58	Yes	HRIFA017791a	0.87	Yes
PLACE1009982	F-PLACE1009982	0.94	Yes	HRIFA018075a	0.94	Yes
PLACE1011236	F-PLACE1011236	0.52	Yes	HRIFA018827a	0.66	Yes
PLACE2000219	F-PLACE2000219	0.73	Yes	HRIFA034010a	0.73	Yes
SKNMC1000004	F-SKNMC1000004	0.94	Yes	HRIFA030097a	0.94	Yes
THYRO1000036	F-THYRO1000036	0.83	Yes	HRIFA027754a	0.83	Yes
THYRO1000099	F-THYRO1000099	0.94	Yes	HRIFA027803a	0.94	Yes
THYRO1001237	F-THYRO1001237	0.94	Yes	HRIFA030248a	0.94	Yes
THYRO1001327	F-THYRO1001327	0.93	Yes	HRIFA025125a	0.94	Yes
THYRO1001495	F-THYRO1001495	0.89	Yes	HRIFA030394a	0.89	Yes
THYRO1001523	F-THYRO1001523	0.71	Yes	HRIFA030408a	0.71	Yes
THYRO1001725	F-THYRO1001725	0.94	Yes	HRIFA029107a	0.94	Yes
Y79AA1000226	F-Y79AA1000226	0.94	Yes	HRIFA027874a	0.94	Yes
Y79AA1000521	F-Y79AA1000521	0.92	Yes	HRIFA027961a	0.92	Yes
Y79AA1000776	F-Y79AA1000776	0.78	Yes	HRIFA028401a	0.78	Yes
Y79AA1000959	F-Y79AA1000959	0.9	Yes	HRIFA028465a	0.9	Yes
Y79AA1001013	F-Y79AA1001013	0.94	Yes	HRIFA011193a	0.94	Yes
Y79AA1001264	F-Y79AA1001264	0.94	Yes	HRIFA028573a	0.94	Yes
Y79AA1001328	F-Y79AA1001328	0.91	Yes	HRIFA028592a	0.91	Yes
Y79AA1001427	F-Y79AA1001427	0.65	Yes	HRIFA028652a	0.65	Yes

3/4 (continued)

Table 10

The 170 clones in which the selectec clones have the maximal ATGpr1 score 0.5 or higher, and were predicted to contain the signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	name of representative sequence	maximal ATGpr1 score	signal
Y79AA1001430	F-Y79AA1001430	0.94	Yes	HRIFA028654a	0.94	Yes
Y79AA1001530	F-Y79AA1001530	0.94	Yes	HRIFA010206a	0.94	Yes
Y79AA1001592	F-Y79AA1001592	0.94	Yes	HRIFA028708a	0.94	Yes
Y79AA1001793	F-Y79AA1001793	0.89	Yes	HRIFA032066a	0.89	Yes
Y79AA1001795	F-Y79AA1001795	0.59	Yes	HRIFA032067a	0.59	Yes
Y79AA1001863	F-Y79AA1001863	0.56	Yes	HRIFA032097a	0.15	Yes
Y79AA1002022	F-Y79AA1002022	0.94	Yes	HRIFA033718a	0.94	Yes
Y79AA1002373	F-Y79AA1002373	0.79	Yes	HRIFA032271a	0.79	Yes

4/4

Table 11

The 35 clones in which the selected clones have the maximal ATGpr1 score 0.3 or higher and less than 0.5, and were predicted to contain the signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	representative sequence	maximal ATGpr1 score	signal
HEMBA1000907	F-HEMBA1000907	0.39	Yes	HRIFA000845a	0.94	Yes
HEMBA1003602	F-HEMBA1003602	0.43	Yes	HRIFA020109a	0.43	Yes
HEMBA1004797	F-HEMBA1004797	0.45	Yes	HRIFA020883a	0.66	Yes
HEMBB1000447	F-HEMBB1000447	0.31	Yes	HRIFA001558a	0.76	Yes
MAMMA1000591	F-MAMMA1000591	0.34	Yes	HRIFA026303a	0.77	Yes
MAMMA1000681	F-MAMMA1000681	0.35	Yes	HRIFA026364a	0.94	Yes
MAMMA1000986	F-MAMMA1000986	0.37	Yes	HRIFA021611a	0.37	Yes
MAMMA1001893	F-MAMMA1001893	0.44	Yes	HRIFA027485a	0.9	Yes
MAMMA1001957	F-MAMMA1001957	0.48	Yes	HRIFA027536a	0.94	Yes
NT2RM2001941	F-NT2RM2001941	0.44	Yes	HRIFA032011a	0.94	Yes
NT2RP1000050	F-NT2RP1000050	0.47	Yes	HRIFA005102a	0.54	Yes
NT2RP1000903	F-NT2RP1000903	0.38	Yes	HRIFA005650a	0.38	Yes
NT2RP2003469	F-NT2RP2003469	0.33	Yes	HRIFA008661a	0.9	Yes
NT2RP2003664	F-NT2RP2003664	0.36	Yes	HRIFA008790a	0.89	Yes
NT2RP2004447	F-NT2RP2004447	0.36	Yes	HRIFA009339a	0.93	Yes
NT2RP2006042	F-NT2RP2006042	0.37	Yes	HRIFA010425a	0.69	Yes
NT2RP3001195	F-NT2RP3001195	0.44	Yes	HRIFA023227a	0.94	Yes
NT2RP3003354	F-NT2RP3003354	0.3	Yes	HRIFA008212a	0.51	Yes
NT2RP3003469	F-NT2RP3003469	0.3	Yes	HRIFA025143a	0.3	Yes
NT2RP3003963	F-NT2RP3003963	0.44	Yes	HRIFA008949a	0.62	Yes
NT2RP3004133	F-NT2RP3004133	0.35	Yes	HRIFA025706a	0.94	Yes
NT2RP3004309	F-NT2RP3004309	0.4	Yes	HRIFA025778a	0.92	Yes
OVARC1000208	F-OVARC1000208	0.4	Yes	HRIFA010942a	0.4	Yes
PLACE1001536	F-PLACE1001536	0.33	Yes	HRIFA012761a	0.31	Yes
PLACE1003407	F-PLACE1003407	0.48	Yes	HRIFA013899a	0.48	Yes
PLACE1003428	F-PLACE1003428	0.37	Yes	HRIFA013911a	0.61	Yes
PLACE1003460	F-PLACE1003460	0.38	Yes	HRIFA013932a	0.94	Yes
PLACE1005569	F-PLACE1005569	0.32	Yes	HRIFA015351a	0.68	Yes
PLACE1006277	F-PLACE1006277	0.32	Yes	HRIFA015802a	0.65	Yes
PLACE1010251	F-PLACE1010251	0.32	Yes	HRIFA018238a	0.62	Yes
THYRO1000196	F-THYRO1000196	0.44	Yes	HRIFA029050a	0.71	Yes
THYRO1000795	F-THYRO1000795	0.33	Yes	HRIFA029327a	0.92	Yes
THYRO1000999	F-THYRO1000999	0.4	Yes	HRIFA030203a	0.4	Yes
THYRO1001478	F-THYRO1001478	0.47	Yes	HRIFA030385a	0.89	Yes
Y79AA1000426	F-Y79AA1000426	0.47	Yes	HRIFA027940a	0.92	Yes

Table 12

41 clones from which selected clones have the maximal ATGpr1 score 0 or higher and less than 0.3, and predicted to be containing the signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	representative sequence	maximal ATGpr1 score	signal
HEMBA1000300	F-HEMBA1000300	0.13	Yes	HRIFA000284a	0.13	Yes
HEMBA1002164	F-HEMBA1002164	0.11	Yes	HRIFA001972a	0.74	Yes
HEMBA1002239	F-HEMBA1002239	0.17	Yes	HRIFA002037a	0.17	Yes
HEMBA1002421	F-HEMBA1002421	0.22	Yes	HRIFA005392a	0.9	Yes
HEMBA1003294	F-HEMBA1003294	0.15	Yes	HRIFA020163a	0.15	Yes
HEMBA1006572	F-HEMBA1006572	0.06	Yes	HRIFA021543a	0.62	Yes
HEMBA1007013	F-HEMBA1007013	0.19	Yes	HRIFA021906a	0.82	Yes
HEMBB1000567	F-HEMBB1000567	0.09	Yes	HRIFA029730a	0.15	Yes
HEMBB1002663	F-HEMBB1002663	0.29	Yes	HRIFA031871a	0.29	Yes
MAMMA1001043	F-MAMMA1001043	0.17	Yes	HRIFA026764a	0.81	Yes
MAMMA1001284	F-MAMMA1001284	0.26	Yes	HRIFA026889a	0.26	Yes
MAMMA1001901	F-MAMMA1001901	0.17	Yes	HRIFA027493a	0.17	Yes
MAMMA1002224	F-MAMMA1002224	0.13	Yes	HRIFA027717a	0.13	Yes
NT2RM2000306	F-NT2RM2000306	0.25	Yes	HRIFA021985a	0.25	Yes
NT2RM2000410	F-NT2RM2000410	0.22	Yes	HRIFA022055a	0.82	Yes
NT2RP2000479	F-NT2RP2000479	0.24	Yes	HRIFA000822a	0.12	Yes
NT2RP2001495	F-NT2RP2001495	0.19	Yes	HRIFA007226a	0.78	Yes
NT2RP2001948	F-NT2RP2001948	0.29	Yes	HRIFA007565a	0.89	Yes
NT2RP3000645	F-NT2RP3000645	0.2	Yes	HRIFA022890a	0.91	Yes
NT2RP3003076	F-NT2RP3003076	0.23	Yes	HRIFA024978a	0.65	Yes
NT2RP4001879	F-NT2RP4001879	0.26	Yes	HRIFA017818a	0.79	Yes
NT2RP4002451	F-NT2RP4002451	0.11	Yes	HRIFA018447a	0.34	Yes
OVARC1000439	F-OVARC1000439	0.15	Yes	HRIFA011105a	0.21	Yes
OVARC1001727	F-OVARC1001727	0.22	Yes	HRIFA019960a	0.22	Yes
PLACE1002080	F-PLACE1002080	0.17	Yes	HRIFA013092a	0.76	Yes
PLACE1002095	F-PLACE1002095	0.23	Yes	HRIFA013103a	0.61	Yes
PLACE1004028	F-PLACE1004028	0.12	Yes	HRIFA014303a	0.12	Yes
PLACE1004482	F-PLACE1004482	0.13	Yes	HRIFA014590a	0.57	Yes
PLACE1005383	F-PLACE1005383	0.11	Yes	HRIFA015219a	0.52	Yes
PLACE1005544	F-PLACE1005544	0.08	Yes	HRIFA009852a	0.41	Yes
PLACE1005660	F-PLACE1005660	0.2	Yes	HRIFA015409a	0.2	Yes
PLACE1006443	F-PLACE1006443	0.27	Yes	HRIFA015902a	0.89	Yes
PLACE1007296	F-PLACE1007296	0.22	Yes	HRIFA016430a	0.27	Yes
PLACE1008469	F-PLACE1008469	0.27	Yes	HRIFA017146a	0.94	Yes
PLACE1008984	F-PLACE1008984	0.11	Yes	HRIFA017456a	0.74	Yes
PLACE4000455	F-PLACE4000455	0.23	Yes	HRIFA012333a	0.51	Yes
SKNMC1000014	F-SKNMC1000014	0.15	Yes	HRIFA030106a	0.76	Yes
THYRO1001702	F-THYRO1001702	0.14	Yes	HRIFA030511a	0.8	Yes
Y79AA1000270	F-Y79AA1000270	0.21	Yes	HRIFA005644a	0.63	Yes
Y79AA1001056	F-Y79AA1001056	0.27	Yes	HRIFA028497a	0.27	Yes
Y79AA1001803	F-Y79AA1001803	0.08	Yes	HRIFA032073a	0.68	Yes

Table 13

Four clones from which selected clones have the maximal ATGpr1 score 0.5 or higher, and predicted to be lacking the signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	name of representative sequence	maximal ATGpr1 score	signal
NT2RP3002281	F-NT2RP3002281	0.81	No	HRIFA012999a	0.61	Yes
NT2RP3002721	F-NT2RP3002721	0.94	No	HRIFA023305a	0.57	Yes
NT2RP3004083	F-NT2RP3004083	0.94	No	HRIFA008387a	0.76	Yes
PLACE1005669	F-PLACE1005669	0.94	No	HRIFA012513a	0.65	Yes

Table 14

Two clones from which selected clones have the maximal ATGpr1 score 0.3 or higher and less than 0.5 and predicted to have no signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	representative sequence	maximal ATGpr1 score	signal
NT2RP3000481	F-NT2RP3000481	0.47	No	HRIFA028614a	0.93	Yes
NT2RP3003559	F-NT2RP3003559	0.48	No	HRIFA025514a	0.45	Yes

Table 15

Two clones from which selected clones have the maximal ATGpr1 score 0 or higher and less than 0.3, and predicted to have no signal sequence by the PSORT

name of clone	name of sequence	maximal ATGpr1 score	signal	representative sequence	maximal ATGpr1 score	signal
PLACE1005601	F-PLACE1005601	0.12	No	HRIFA010593a	0.64	Yes
PLACE1006786	F-PLACE1006786	0.22	No	HRIFA012333a	0.51	Yes

EXAMPLE 12

A method for the selection of clones based on the top hit data in the homology search against the SwissProt (a method for the selection of a novel full-length protein that is predicted to have a function based on the top hit data).

[0176] The representative sequences of the clusters were discarded in which the 5'-end sequence is identical (90% or more matching), or not similar (the compared part contains a sequence of 25 nucleotides or shorter and the similarity is lower than 60%) to the top hit data in the SwissProt. Then, the remaining representative sequences which has similarity to the representative sequences of the 5'-ends were classified by a group of the above keywords (some representative sequences belong to a group by multiple keywords), and then clones were selected from the clusters. The names and the corresponding SEQ IDs of the representative sequences, and also the names of the introns (including the representative sequence of the 5'-end or the 3'-end, or ESTs) used for selecting the clones from the representative sequences and the corresponding SEQ IDs are shown in the last part of the present specification (Table 368 and 369, respectively). HRIFA indicates the representative sequence of the 5'-end group, and HRIRA indicates the representative sequence of the 3'-end group.

[0177] In principle, from the clusters containing only a single clone (the 5'-end sequence is the representative sequence of the cluster), the clone was selected. However, in the following cases, the clone containing a longer 5'-end was selected: where the maximal ATGpr1 score was less than 0.5, the 5'-end sequence of the clone to be selected was not complete, or the 5'-end of the clone was found to be obviously short nevertheless the clone should not be

included in the same cluster based on the BLAST analysis between the other clones, or further, the 5'-end sequence of the said clone, which corresponds to the 3'-ends of the other clones belonging to the same cluster in which the 3'-end of the said clone was included, was turn out to be longer than those of the other clones by assembling them. When there were two clones in the same cluster, judged to be full-length, and it was difficult to determine which clone has the longer 5'-end even by assembling them, all the clones were selected. As a result, the ATGpr1 score in some clones became less than 0.5 or less than 0.3. The fullness ratio of these clones became lower, but there is still a possibility that the clones are full-length.

[0178] In the case in which multiple clones were contained in a cluster, selected was the clone having the longest 5'-end in the clones judged to be full-length compared to the human mRNA or human EST. However, in the following cases, the clone containing a longer 5'-end was selected: where the maximal ATGpr1 score was less than 0.5, the 5'-end sequence of the clone to be selected was not complete, or the 5'-end of the clone was found to be obviously short nevertheless the clone should not be included in the same cluster based on the BLAST analysis between the other clones, or further, the 5'-end sequence of the said clone, which corresponds to the 3'-ends of the other clones belonging to the same cluster in which the 3'-end of the said clone was included, was turn out to be longer than those of the other clones by assembling them. When there were two clones in the same cluster, judged to be full-length, and it was difficult to determine which clone has the longer 5'-end even by assembling them, all the clones were selected. As a result, the ATGpr1 score in some clones became less than 0.5 or less than 0.3. These clones can still be full-length.

[0179] Based on the top hit data in the SwissProt homology search, 658 clones were selected. Among them, 446 clones were selected by the keywords, secretion or membrane. Using the keyword, glycoprotein, 243 clones were selected. 51 clones were selected by the keywords for signal transduction. With the keywords for transcription, 130 clones were selected. 17 clones were selected by the keywords for disease.

[0180] Among the 446 clones selected by the keywords, secretion or membrane, 77 clones were overlapped with those selected by combining the ATGpr1 score and prediction by the PSORT for the existence of a signal sequence. Also, many clones were overlapped with those selected by the keyword, glycoprotein. Moreover, some clones were overlapped with the clones selected by the keywords for diseases.

[0181] Among the 243 clones selected by the keyword, glycoprotein, 53 clones were overlapped with those selected by combining the ATGpr1 score and prediction by the PSORT for the existence of a signal sequence. Also, many clones were overlapped with those selected by the keywords, secretion or membrane. Moreover, some clones were overlapped with the clones selected by the keywords in diseases.

[0182] Among the clones selected by the top hit data in the homology search on the SwissProt, 532 clones were having the maximal ATGpr1 score 0.5 or higher. 59 clones were having the maximal score 0.3 or higher and less than 0.5. 67 clones were with the maximal score less than 0.3.

[0183] When the maximal ATGpr1 score is 0.5 or higher, 0.3 or higher, no less than 0, the expected fullness ratio is as shown in Table 3, 4, 5, and 6, respectively.

Table 16

The representative sequences of the most homologous sequences in the SwissProt with the keyword(s) "growth factor", "cytokine", or "hormone", and the selected clones.

name of clone	name of representative sequence
HEMBA1001563	HRIFA001439a
HEMBA1003047	HRIFA002743a
HEMBA1005070	HRIFA020144a
HEMBA1006724	HRIFA021620a
HEMBA1006916	HRIFA021855a
MAMMA1001066	HRIFA027355a
MAMMA1001634	HRIFA027187a
MAMMA1002165	HRIFA027673a
NT2RM4000326	HRIFA032530a
NT2RM4001377	HRIFA005300a
NT2RP2000447	HRIFA006448a
NT2RP2000663	HRIFA006609a
NT2RP2000903	HRIFA006798a
NT2RP2002974	HRIFA027860a
NT2RP2003369	HRIFA008596a
NT2RP2004141	HRIFA009123a

EXAMPLE 13

Selection of cDNA clone NT2RP2036580

[0184] Clone NT2RP2006580 as well as clone HEMBA1000121 was selected from the representative sequences belonging to HRIFA000116a cluster of the most homologous sequence in the SwissProt with the keywoods "transmembrane". Although each of the clones, HEMBA1000121 and NT2RP2006580, was assembled with other clones for 5' extension, any other clones did not extend the clones toward the 5' direction. Accordingly, it is possible that both clones are full-length cDNA clones. The maximal ATGpr1 score of F-NT2RP2006580 is 0.37, and therefore, the fullness ratio is low. However, it is still possible for the sequence to cover the full-length.

[0185] Thus, the total number of selected clones is 830. Based on the top matching data resulted from Swiss-Prot homology search, 659 clones were selected. From them, 447 clones were selected by the keywords of "secretion" and "membrane". Among the clones selected based on the top matching data, 60 clones exhibited the maximal ATGpr1 score of 0.3 or higher and less than 0.5.

[0186] The sequences of F-NT2RP2006580 and R-NT2RP2006580 are shown in SEQ ID NO: 2545 and SEQ ID NO: 2546, respectively.

EXAMPLE 14

Full-length sequence analysis and homology search

[0187] Full-length sequence was determined for each selected cDNA clones. The nucleotide sequence determination was performed mainly by the dye-terminator method using custom synthesized DNA primers according to the primer walking procedure (custom synthesized DNA primers were used for sequencing; sequencing reaction was performed with DNA sequencing reagent supplied by PE Biosystems according to the supplier's manual; and the samples were analyzed in an automatic sequencer made by the same supplier). Sequence determination of some clones was carried out in the same manner but using a Licor DNA sequencer. Overlapping partial nucleotide sequences, which were obtained by the above-described method, were assembled together to determine a full-length nucleotide sequence. Amino acid sequences were then deduced from the determined full-length nucleotide sequences. However, amino acid sequence is not shown for a clone of which coding region was hard to be deduced or of which amino acid sequence has less than 100 amino acid residues. SEQ ID NOs corresponding to the respective clones are indicated in Table 370.

[0188] GenBank, Swiss-Prot and UniGene were searched for the determined nucleotide sequences by BLAST analysis. Matching data of cDNA clone which exhibits higher homology and of which functions are easily predicted based on the nucleotide sequences and the deduced amino acid sequences are selected from the BLAST analysis matching data with P value of 10^{-4} or less. The matching data selected are listed herein. However, there are some clones that did not match the criteria for judgment and such matching data of BLAST analysis are not shown herein. The results of homology search indicated in the last part of this specification are as follows.

[0189] Homology search result 1: data obtained by the homology search of Swiss-Prot database for representative sequences of the 5'-end cluster

[0190] Homology search result 2: homology of representative sequences of the 5'-end cluster to the data in Swiss-Prot database; the P value is 10^{-10} or less

[0191] Homology search result 3: homology of representative sequences of the 5'-end cluster to the data in Swiss-Prot database; the P value is higher than 10^{-10} and 10^{-4} or less

[0192] Homology search result 4: homology of representative sequences of the 5'-end cluster to the data in Swiss-Prot database; the P value is higher than 10^{-4} and 1 or less

[0193] Homology search result 5: data obtained by the homology search of Swiss-Prot database for 5'-end sequences of cDNA clone

[0194] Homology search result 6: data obtained by the homology search of GenBank database (http://www.ncbi.nlm.nih.gov/web/GenBank/) except for EST and STS sequence data for 5'-end sequences of cDNA clone

[0195] Homology search result 7: data obtained by the homology search of GenBank database (http://www.ncbi.nlm.nih.gov/web/GenBank/) except for EST and STS sequence data for 3'-end sequences of cDNA clone

[0196] Homology search result 8: data obtained by the homology search of Human UniGene database (http://www.ncbi.nlm.nih.gov/Unigene) for 5'-end sequences of cDNA clone

[0197] Homology search result 9: data obtained by the homology search of Human UniGene database (http://www.ncbi.nlm.nih.gov/Unigene) for 3'-end sequences of cDNA clone

[0198] Homology search result 10: result obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences

[0199] The P value indicates similarity between two sequences as a score by considering the probability that the two

sequences are accidentally similar. In general, as the value is lower, the similarity is higher. In general, as the value is lower, the homology is higher (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.L. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

Example 15. Gene expression analysis with hybridization using high density DNA filter

[0200] Nylon membrane for DNA spotting was prepared according to the following procedure. E. coli was cultured in each well of a 96-well plate (in a LB medium at 37. for 16 hours). A sample of each culture was suspended in 10 . 1 of sterile water in a well of a 96-well plate. The plate was heated at 100. for 10 minutes. Then, the boiled samples were analyzed by PCR. PCR was performed in a 20 .1 solution by using TaKaRa PCR Amplification Kit (Takara) according to the supplier's protocol. Primers used for the amplification of an insert cDNA in a plasmid were a pair of sequencing primers, ME761FW (5' tacggaagtgttacttctgc 3'/ SEQ ID NO: 3591) and ME1250RV (5' tgtgggaggtttttttctcta 3'/ SEQ ID NO: 3592), or a pair of primers, M13M4 (5' gttttcccagtcacgac 3'/ SEQ ID NO: 3593) and M13RV (5' caggaaacagctatgac 3' / SEQ ID NO: 3594). PCR was performed using a thermal cycler, GeneAmp System 9600 (PE Biosystems) at 95. for 5 minutes; at 95. for 10 seconds and at 68. for 1 minute for 10 cycles; at 98. for 20 seconds and at 60. for 3 minutes for 20 cycles; and at 72. for 10 minutes. After the PCR, the 20 .1 reaction solution was loaded onto a 1% agarose gel and fractionated by electrophoresis. DNA on the gel was stained with ethidium bromide to confirm the amplification of cDNA. When cDNAs were not amplified by PCR, plasmids containing the corresponding insert cDNAs were prepared by the alkali-extraction method (J. Sambrook, E.F., Fritsh, & T. Maniatis, "Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989).

[0201] Preparation of DNA array was carried out by the following procedure. A sample of a DNA solution was added in each well of a 384-well plate. DNA was spotted onto a nylon membrane (Boehringer) by using a 384-pin tool of Biomek 2000 Laboratory Automation System (Beckman-Coulter). Specifically, the 384-well plate containing the DNA was placed under the 384-pin tool. The independent 384 needles were simultaneously dipped into the DNA solution for DNA deposition. The needles were gently pressed onto a nylon membrane and the DNA deposited at the tips of needles was spotted onto the membrane. Denaturation of the spotted DNA and immobilization of the DNA on the nylon membrane were carried out according to standard methods (J. Sambrook, E.F., Fritsh, & T. Maniatis, "Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989).

[0202] A probe for hybridization was radioisotope-labeled first strand cDNA. Synthesis of the first strand cDNA was performed by using Thermoscript(TM) RT-PCR System (GIBCO). Specifically, the first strand cDNA was synthesized by using 1.5 .g of mRNAs from various human tissues (Clontech), 1 .1 of 50.M Oligo(dT)20 and 50.Ci [.^{33}P]dATP according to an attached protocol. Purification of a probe was carried out by using ProbeQuant(TM) G-50 micro column (Amersham-Pharmacia Biotech) according to an attached protocol. In the next step, 2 units of E. coli RNase H were added to the reaction mixture. The mixture was incubated at room temperature for 10 minutes, and then, 100.g of human COT-1 DNA (GIBCO) was added thereto. The mixture was incubated at 97. for 10 minutes and then was allowed to stand on ice to give hybridization probe.

[0203] Hybridization of the radioisotope-labeled probe to the DNA array was performed according to standard methods (J. Sambrook, E.F., Fritsh, & T. Maniatis, Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989). The membrane was washed as follows: the nylon membrane was washed 3 times by incubating it in Washing solution 1 (2xSSC, 1% SDS) at room temperature (about 26.) for 20 minutes; then the membrane was washed 3 times by incubating it in Washing solution 2 (0.1xSSC, 1% SDS) at 65. for 20 minutes.

[0204] Autoradiography was performed by using an image plate for BAS2000 (Fuji Photo Film Co., Ltd.). Specifically, the nylon membrane with probe hybridized thereon was wrapped with a piece of Saran Wrap and brought into tight contact with the image plate on the light-sensitive surface. The membrane with the image plate was placed in an imaging cassette for radioisotope and allowed to stand in dark place for 4 hours. The radioactivity recorded on the image plate was analyzed by using BAS2000 (Fuji Photo Film Co., Ltd.). The activity was subjected to electronic conversion and recorded as an image file of autoradiogram. The signal intensity of each DNA spot was analyzed by using Visage High Density Grid Analysis Systems (Genomic Solutions Inc.). The signal intensity was converted into numerical data. The data were taken in duplicate. The reproducibility was assessed by comparing the signal intensities of the corresponding spots on the duplicated DNA filters that were hybridized to a single DNA probe (Figure 2). In 95% of entire spots, the ratio between the corresponding spots falls within a range of 2 or less, and the correlation coefficient is r=1.97. Thus, the reproducibility is satisfactory.

[0205] The detection sensitivity in gene expression analysis was estimated by examining increases in the signal intensity of probe concentration-dependent spot in hybridization using a probe complementary to the DNA spotted on the nylon membrane. DNA used was PLACE 1008092 (the same as DNA deposited in GenBank under an Accession No. AF107253). The DNA array with DNA of PLACE1008092 was prepared according to the above-mentioned method. The probe used was prepared as follows: mRNA was synthesized in vitro from the clone, PLACE1008092. By using

this mRNA as a template, radioisotope-labeled first strand cDNA was synthesized in the same manner as described above, and the cDNA was used as the probe. In order to synthesize mRNA from PLACE1008092 in vitro, a plasmid in which the 5' end of the cDNA PLACE1008092 was ligated to the T7 promoter of pBluescript SK(-) was constructed. Specifically, the PLACE1008092 insert was cut out from pME18SFL3 carrying the cDNA at a DralII site thereof by XhoI digestion. The resulting PLACE1008092 fragment was ligated to XhoI-predigested pBluescript SK(-) by using DNA ligation kit ver.2 (Takara). The in vitro mRNA synthesis from PLACE1008092 inserted into pBluescript SK(-) was carried out by using Amplischribe(TM) T7 high yield transcription kit (Epicentre technologies). Hybridization and the analysis of signal intensity of each DNA spot were performed by the same methods as described above. When the probe concentration is $1x10^7$ g/ml or less, there was no increase of signal intensity proportional to the probe concentration. Therefore, it was assumed to be difficult to compare the signals with one another in this concentration range. Thus, the spots with the intensity of 40 or less were uniformly taken as low level signals (Figure 3). Within a concentration of the probe ranging from $1x10^7$ g/ml to 0.1 g/ml, the signal was found to increase in a probe concentration-dependent manner. The detection limit represented as the ratio of the expression level of test mRNA to that of total mRNA in a sample was 1:100,000.

[0206] Tables 28-184 (also containing clones without description in Examples) show the expression of each cDNA in human normal tissues (heart, lung, pituitary gland, thymus, brain, kidney, liver and spleen). The expression levels are indicated with numerical values of 0-10,000. Genes that were expressed in at least a single tissue are indicated below by the corresponding clone names:

clone: BNGH41000020, BNGH41000087, BNGH41000091, HEMBA1000121, HEMBA1000275, HEMBA1000300, HEMBA1000443, HEMBA1000462, HEMBA1000477, HEMBA1000634, HEMBA1000713, HEMBA1000835, HEMBA1000875, HEMBA1000940, HEMBA1000962, HEMBA1001228, HEMBA1001296, HEMBA1001390, HEMBA1001563, HEMBA1001621, HEMBA1002048, HEMBA1002131, HEMBA1002163, HEMBA1002164, HEMBA1002167, HEMBA1002178, HEMBA1002195, HEMBA1002227, HEMBA1002239, HEMBA1002316, HEMBA1002421, HEMBA1002524, HEMBA1002551, HEMBA1002767, HEMBA1002985, HEMBA1002992, HEMBA1003047, HEMBA1003072, HEMBA1003101, HEMBA1003120, HEMBA1003230, HEMBA1003294, HEMBA1003315, HEMBA1003392, HEMBA1003399, HEMBA1003487, HEMBA1003530, HEMBA1003945, HEMBA1004007, HEMBA1004067, HEMBA1001085, HEMBA1004110, HEMBA1004391, HEMBA1004444, HEMBA1004454, HEMBA1004505, HEMBA1004797, HEMBA1004952, HEMBA1005070, HEMBA1005084, HEMBA1005145, HEMBA1005230, HEMBA1005246, HEMBA1005337, HEMBA1005430, HEMBA1005449, HEMBA1005489, HEMBA1005545, HEMBA1005698, HEMBA1005929, HEMBA1005945, HEMBA1005016, HEMBA1006171, HEMBA1006276, HEMBA1006311, HEMBA1006335, HEMBA1006357, HEMBA1006430, HEMBA1006482, HEMBA1006517, HEMBA1006544, HEMBA1006658, HEMBA1006707, HEMBA1006749, HEMBA1006770, HEMBA1006902, HEMBA1006912, HEMBA1006916, HEMBA1006960, HEMBA1007013, HEMBA1007057, HEMBA1007063, HEMBA1007291, HEMBA1007332, HEMBB1000106, HEMBB1000309, HEMBB1000447, HEMBB1000542, HEMBB1000567, HEMBB1000642, HEMBB1000905, HEMBB1001026, HEMBB1001048, HEMBB1001407, HEMBB1001530, HEMBB1001573, HEMBB1001847, HEMBB1001959, HEMBB1001978, HEMBB1002039, HEMBB1002041, HEMBB1002051, HEMBB1002162, HEMBB1002228, HEMBB1002302, HEMBB1002427, HEMBB1002465, HEMBB1002661, HEMBB1002663, HEMBB1002693, MAMMA1000046, MAMMA1000102, MAMMA1000106, MAMMA1000118, MAMMA1000204, MAMMA1000226, MAMMA1000403, MAMMA1000449, MAMMA1000457, MAMMA1000473, MAMMA1000528, MAMMA1000591, MAMMA1000614, MAMMA1000652, MAMMA1000681, MAMMA1000706, MAMMA1000788, MAMMA1000810, MAMMA1000814, MAMMA1000881, MAMMA1000986, MAMMA1000994, MAMMA1001043, MAMMA1001066, MAMMA1001094, MAMMA1001141, MAMMA1001150, MAMMA1001284, MAMMA1001310, MAMMA1001344, MAMMA1001418, MAMMA1001532, MAMMA1001609, MAMMA1001615, MAMMA1001634, MAMMA1001893, MAMMA1001901, MAMMA1001957, MAMMA1002070, MAMMA1002091, MAMMA1002095, MAMMA1002128, MAMMA1002142, MAMMA1002165, MAMMA1002205, MAMMA1002224, MAMMA1002586, MAMMA1003126, NT2RM1000407, NT2RM1000462, NT2RM1000542, NT2RM1000789, NT2RM1000855, NT2RM1000858, NT2RM2000241, NT2RM2000306, NT2RM2000410, NT2RM2000423, NT2RM2000497, NT2RM2000514, NT2RM2000565, NT2RM2000582, NT2RM2000589, NT2RM2000622, NT2RM2000773, NT2RM2001126, NT2RM2001626, NT2RM2001792, NT2RM2001941, NT2RM4000198, NT2RM4000295, NT2RM4000444, NT2RM4000593, NT2RM4000761, NT2RM4000965, NT2RM4000997, NT2RM4001321, NT2RM4001325, NT2RM4001377, NT2RM4001735, NT2RM4001768, NT2RM4001843, NT2RP1000002, NT2RP1000181, NT2RP1000271, NT2RP1000300, NT2RP1000325, NT2RP1000465, NT2RP1000468, NT2RP1000740, NT2RP1000903, NT2RF1000981, NT2RP2000092, NT2RP2000178, NT2RP2000240, NT2RP2000447, NT2RP2000479, NT2RP2000533, NT2RP2000610, NT2RP2000616, NT2RP2000694, NT2RP2000739, NT2RP2001200, NT2RP2001223, NT2RP2001388, NT2RP2001469, NT2RP2001480, NT2RP2001514, NT2RP2001529, NT2RP2001538, NT2RP2001562, NT2RP2001662, NT2RP2001878, NT2RP2001903,

NT2RP2001921, NT2RP2001956, NT2RP2002015, NT2RP2002063, NT2RP2002188, NT2RP2002232, NT2RP2002409, NT2RP2002510, NT2RP2002527, NT2RP2002533, NT2RP2002564, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002974, NT2RP2003138, NT2RP2003179, NT2RP2003210, NT2RP2003302, NT2RP2003369, NT2RP2003383, NT2RP2003390, NT2RP2003469, NT2RP2003593, NT2RP2003599, NT2RP2003655, NT2RP2003940, NT2RP2003950, NT2RP2004069, NT2RP2004108, NT2RP2004141, NT2RP2004179, NT2RP2004205, NT2RP2004447, NT2RP2004524, NT2RP2004556, NT2RP2004606, NT2RP2004648, NT2RP2004794, NT2RP2004837, NT2RP2004847, NT2RP2005027, NT2RP2005069, NT2RP2005163, NT2RP2005181, NT2RP2005247, NT2RP2005378, NT2RP2005391, NT2RP2005425, NT2RP2005463, NT2RP2005535, NT2RP2005541, NT2RP2005597, NT2RP2005632, NT2RP2005666, NT2RP2005774, NT2RP2005878, NT2RP2005887, NT2RP2005941, NT2RP2006004, NT2RP2006042, NT2RP2006092, NT2RP2006099, NT2RP2006269, NT2RP3000011, NT2RP3000022, NT2RP3000059, NT2RP3000063, NT2RP3000125, NT2RP3000148, NT2RP3000171, NT2RP3000172, NT2RP3000201, NT2RP3000232, NT2RP3000304, NT2RP3000378, NT2RP3000436, NT2RP3000460, NT2RP3000645, NT2RP3000652, NT2RP3000676, NT2RP3000677, NT2RP3000721, NT2RP3000789, NT2RP3000818, NT2RP3000820, NT2RP3000838, NT2RP3000907, NT2RP3000921, NT2RP3001044, NT2RP3001159, NT2RP3001170, NT2RP3001195, NT2RP3001271, NT2RP3001388, NT2RP3001560, NT2RP3001592, NT2RP3001685, NT2RP3001738, NT2RP3001754, NT2RP3001858, NT2RP3001976, NT2RP3002015, NT2RP3002160, NT2RP3002281, NT2RP3002311, NT2RP3002324, NT2RP3002353, NT2RP3002409, NT2RP3002411, NT2RP3002721, NT2RP3002737, NT2RP3002738, NT2RP3002836, NT2RP3002900, NT2RP3002958, NT2RP3003000, NT2RP3003076, NT2RP3003354, NT2RP3003448, NT2RP3003469, NT2RP3003473, NT2RP3003532, NT2RP3003614, NT2RP3003729, NT2RP3003849, NT2RP3003874, NT2RP3003939, NT2RP3003963, NT2RP3004025, NT2RP3004067, NT2RP3004083, NT2RP3004090, NT2RP3004119, NT2RP3004130, NT2RP3004133, NT2RP3004202, NT2RP3004294, NT2RP3004309, NT2RP3004321, NT2RP3004355, NT2RP3004374, NT2RP3004406, NT2RP3004481, NT2RP3004552, NT2RP3004557, NT2RP3004625, NT2RP3004640, NT2RP3004647, NT2RP4000108, NT2RP4000634, NT2RP4001877, NT2RP4001879, NT2RP4002187, NT2RP4002715, NT2RP4002750, OVARC1000090, OVARC1000105, OVARC1000137, OVARC1000208, OVARC1000255, OVARC1000313, OVARC1000331, OVARC1000410, OVARC1000439, OVARC1000467, OVARC1000529, OVARC1000553, OVARC1000775, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000956, OVARC1000995, OVARC1001030, OVARC1001049, OVARC1001086, OVARC1001163, OVARC1001260, OVARC1001336, OVARC1001569, OVARC1001570, OVARC1001596, OVARC1001807, OVARC1001833, OVARC1001991, PLACE1000231, PLACE1000258, PLACE1000442, PLACE1000560, PLACE1000912, PLACE1000927, PLACE1001016, PLACE1001100, PLACE1001114, PLACE1001183, PLACE1001229, PLACE1001340, PLACE1001407, PLACE1001500, PLACE1001516, PLACE1001655, PLACE1001836, PLACE1001918, PLACE1002080, PLACE1002095, PLACE1002153, PLACE1002329, PLACE1002374, PLACE1002518, PLACE1002547, PLACE1002726, PLACE1002905, PLACE1002911, PLACE1002967, PLACE1003163, PLACE1003407, PLACE1003428, PLACE1003438, PLACE1003460, PLACE1003529, PLACE1003598, PLACE1003644, PLACE1003772, PLACE1003839, PLACE1003845, PLACE1003852, PLACE1004078, PLACE1004166, PLACE1004168, PLACE1004199, PLACE1004279, PLACE1004282, PLACE1004305, PLACE1004441, PLACE1004482, PLACE1004492, PLACE1004520, PLACE1004630, PLACE1004637, PLACE1004648, PLACE1004816, PLACE1004887, PLACE1005005, PLACE1005031, PLACE1005383, PLACE1005410, PLACE1005426, PLACE1005539, PLACE1005544, PLACE1005569, PLACE1005725, PLACE1005736, PLACE1005768, PLACE1005815, PLACE1005878, PLACE1005927, PLACE1006071, PLACE1006073, PLACE1006079, PLACE1006277, PLACE1006443, PLACE1006716, PLACE1006809, PLACE1007077, PLACE1007096, PLACE1007626, PLACE1007702, PLACE1008469, PLACE1008985, PLACE1009067, PLACE1009527, PLACE1009982, PLACE1010078, PLACE1010251, PLACE1010445, PLACE1011045, PLACE1011116, PLACE1011181, PLACE1011236, PLACE1011364, PLACE1011516, PLACE1011708, PLACE1011978, PLACE2000118, PLACE2000219, PLACE3000181, PLACE4000354, PLACE4000455, SKNMC1000014, THYRO1000061, THYRO1000099, THYRO1000584, THYRO1000795, THYRO1000866, THYRO1000999, THYRO1001063, THYRO1001113, THYRO1001128, THYRO1001205, THYRO1001237, THYRO1001242, THYRO1001456, THYRO1001457, THYRO1001478, THYRO1001495, THYRO1001523, THYRO1001529, THYRO1001593, THYRO1001608, THYRO1001700, THYRO1001702, THYRO1001725, THYRO1001770, THYRO1001803, Y79AA1000127, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1000426, Y79AA1000521, Y79AA1000776, Y79AA1000777, Y79AA1000888, Y79AA1000967, Y79AA1001013, Y79AA1001090, Y79AA1001272, Y79AA1001328, Y79AA1001426, Y79AA1001427, Y79AA1001430, Y79AA1001523, Y79AA1001530, Y79AA1001592, Y79AA1001727, Y79AA1001787, Y79AA1001793, Y79AA1001799, Y79AA1001803, Y79AA1001863, Y79AA1002022, Y79AA1002213, Y79AA1002373, Y79AA1002376, Y79AA1002381.

[0207] Genes that were expressed in all the tissues tested are indicated below by the corresponding clone names: clone: BNGH41000020, HEMBA1000300, HEMBA1001390, HEMBA1002239, HEMBA1002316, HEMBA1004007, HEMBA1004067, HEMBA1005145, HEMBA1005230, HEMBA1005929, HEMBA1006357, HEMBA1006482, HEMBB1000567, HEMBB1001847, NEMBB1001978, MAMMA1000614, MAMMA1000652, MAMMA1000810, MAMMA1000814, MAMMA1001066, MAMMA1001094, MAMMA1001284, MAMMA1001310, MAMMA1001634, MAMMA1002165, MAMMA1002205, MAMMA1002224, NT2RM1000462, NT2RM1000855, NT2RM1000858, NT2RM2000423, NT2RM4000761, NT2RM4000997, NT2RP1000271, NT2RP1000325, NT2RP1000465, NT2RP2001538, NT2RP2001662, NT2RP2001903, NT2RP2002015, NT2RP2002188, NT2RP2002409, NT2RP2002510, NT2RP2002533, NT2RP2004556, NT2RP2004794, NT2RP2004847, NT2RP2005069, NT2RP2005163, NT2RP2005535, NT2RP2006269, NT2RP3000171, NT2RP3000645, NT2RP3000838, NT2RP3001271, NT2RP3001754, NT2RP3003076, NT2RP3003354, NT2RP3003614, NT2RP3004640, NT2RP3004647, OVARC1000090, OVARC1000208, OVARC1000553, OVARC1000995, OVARC1001030, OVARC1001049, PLACE1000231, PLACE1000258, PLACE1001516, PLACE1002080, PLACE1002911, PLACE1003598, PLACE1004648, PLACE1006443, PLACE1008469, PLACE1011708, PLACE2000118, THYRO1001128, THYRO1001205, THYRO1001242, THYRO1001803, Y79AA1000207, Y79AA1001013, Y79AA1001272, Y79AA1001328, Y79AA1001793, Y79AA1001863, Y79AA1002022, Y79AA1002376.

[0208] Genes that were expressed at low levels in any of the tissues tested are indicated below by the corresponding clone names: clone: HEMBA1000006, HEMBA1000128, HEMBA1000349, HEMBA1000590, HEMBA1000671, HEMBA1000732, HEMBA1000745, HEMBA1000907, HEMBA1001184, HEMBA1001221, HEMBA1001272, HEMBA1001297, HEMBA1001878, HEMBA1001886, HEMBA1002420, HEMBA1003497, HEMBA1003602, HEMBA1003732, HEMBA1004250, HEMBA1004785, HEMBA1004971, HEMBA1004982, HEMBA1005267, HEMBA1005522, HEMBA1005913, HEMBA1006299, HEMBA1006572, HEMBA1006724, HEMBA1007241, HEMBB1000276, HEMBB1000407, HEMBB1000668, HEMBB1000679, HEMBB1000881, HEMBB1001200, HEMBB1001547, HEMBB1002120, HEMBB1002245, MAMMA1000141, MAMMA1000496, MAMMA1001237, MAMMA1001623, MAMMA1001978, MAMMA1002080, MAMMA1002087, MAMMA1002234, MAMMA1002633, NT2RM1000580, NT2RM1000899, NT2RM2000632, NT2RM2001643, NT2PM2001818, NT2RM2001902, NT2RM2001939, NT2RM4000100, NT2RM4000115, NT2RM4000284, NT2RM4000326, NT2RM4000417, NT2RM4000587, NT2RM4000648, NT2RM4002352, NT2RP1000050, NT2RP1000239, NT2RP1000261, NT2RP1000448, NT2RP1000551, NT2RP1000579, NT2RP1000613, NT2RP1000679, NT2RP1001004, NT2RP1001020, NT2RP1001031, NT2RP1001563, NT2RP2000394, NT2RP2000514, NT2RP2000649, NT2RP2000663, NT2RP2000712, NT2RP2000818, NT2RP2000903, NT2RP2001276, NT2RP2001495, NT2RP2001755, NT2RP2001769, NT2RP2001817, NT2RP2001915, NT2RP2001948, NT2RP2002304, NT2RP2002674, NT2RP2002976, NT2RP2003042, NT2RP2003545, NT2RP2003664, NT2RP2003931, NT2RP2004495, NT2RP2004670, NT2RP2005514, NT2RP2005883, NT2RP2005994, NT2RP2006134, NT2RP2006512, NT2RP3000169, NT2RP3000444, NT2RP3000481, NT2RP3000616, NT2RP3000871, NT2RP3001012, NT2RP3001061, NT2RP3001240, NT2RP3001322, NT2RP3001542, NT2RP3002286, NT2RP3002342, NT2RP3002448, NT2RP3002571, NT2RP3002664, NT2RP3002790, NT2RP3002887, NT2RP3002983, NT2RP3003527, NT2RP3003535, NT2RP3003559, NT2RP3004000, NT2RP3004075, NT2RP3004345, NT2RP4000962, NT2RP4001001, NT2RP4001009, NT2RP4001467, NT2RP4002451, OVARC1000003, OVARC1000275, OVARC1000298, OVARC1000307, OVARC1000811, OVARC1001132, OVARC1001222, OVARC1001338, OVARC1001607, OVARC1001725, OVARC1001727, OVARC1002058, OVARC1002178, PLACE1000033, PLACE1000740, PLACE1000914, PLACE1000986, PLACE1000123, PLACE1001231, PLACE1001401, PLACE1001464, PLACE1001536, PLACE1001564, PLACE1001788, PLACE1001795, PLACE1001949, PLACE1002355, PLACE1003135, PLACE1003573, PLACE1003737, PLACE1004028, PLACE1004450, PLACE1004519, PLACE1005003, PLACE1005239, PLACE1005250, PLACE1005519, PLACE1005601, PLACE1005660, PLACE1005669, PLACE1005682, PLACE1005745, PLACE1006093, PLACE1006208, PLACE1006219, PLACE1006290, PLACE1006515, PLACE1006786, PLACE1006959, PLACE1007028, PLACE1007040, PLACE1007081, PLACE1007296, PLACE1007591, PLACE1007845, PLACE1007881, PLACE1007971, PLACE1008282, PLACE1008297, PLACE1008359, PLACE1008549, PLACE1008657, PLACE1008716, PLACE1008744, PLACE1008984, PLACE1009196, PLACE1009279, PLACE1009546, PLACE1009600, PLACE1009735, PLACE1010011, PLACE1010081, PLACE1010713, PLACE1010784, PLACE1010827, PLACE1010968, PLACE1011407, PLACE1011824, PLACE3000213, SKNMC1000004, SKNMC1000082, THYRO1000036, THYRO1000196, THYRO1000400, THYRO1000580, THYRO1000678, THYRO1000776, THYRO1000846, THYRO1000956, THYRO1001071, THYRO1001102, THYRO1001266, THYRO1001327, THYRO1001471, Y79AA1000876, Y79AA1000959, Y79AA1001056, Y79AA1001062, Y79AA1001264, Y79AA1001795.

[0209] Genes exhibiting characteristic features in the expression thereof were selected by statistical analysis of these

data. Two examples are shown below to describe the selection of genes of which expression is varied greatly among tissues. The .-actin gene is used frequently as a control in gene expression analysis. Genes of which expression is varied greatly among tissues as compared that of the .-actin gene were determined as follows. Specifically, sum of squared deviation was calculated in the signal intensity of .-actin observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_a^2. Next, sum of squared deviation was calculated in the signal intensity of a compared gene in each tissue, which was divided by 7 degrees of freedom to determine a variance S_b^2. By taking variance ratio F as $F=S_b^2/S_a^2$, genes with a significance level of 5% or more were extracted in the F distribution. Genes extracted are indicated below by the corresponding clone names: clone: BNGH41000020, NT2RM4000761, Y79AA1002376.

[0210] Gene of OVARC1000037(heterogeneous nuclear ribonucleoprotein (hnRNP)) which expression is varied little. Genes of which expression is varied greatly among tissues as compared that of the OVARC1000037 gene were determined as follows. Specifically, sum of squared deviation was calculated in the signal intensity of .-actin observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_a^2. Next, sum of squared deviation was calculated in the signal intensity of a gene to be compared observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_b^2. By taking variance ratio F as $F=S_b^2/S_a^2$, genes with a significance level of 5% or more were extracted in the F distribution. Genes extracted are indicated below by the corresponding clone names: clone: BNGH41000020, HEMBA1000300, OVARC1001030, NT2RM4000761, PLACE1000231, HEMBA1002316, NT2RP1000325, NT2RP1000271, PLACE1004648, HEMBA1005145, HEMBA1005929, NT2RP2002510, NT2RP2001538, NT2RP2002409, NT2RP2002188, NT2RP2001903, NT2RP2002533, NT2RP2002015, NT2RP2006269, NT2RP2004837, NT2RP2004205, NT2RP2005378, HEMBA1006357, HEMBB1000567, NT2RP2003940, NT2RP2004794, HEMBA1006912, NT2RP2004556, NT2RP2005163, NT2RP3000838, NT2RP3001271, PLACE2000118, NT2RP3000645, NT2RP3003076, HEMBB1002693, MAMMA1000046, NT2RP3003354, THYR01001205, MAMMA1000614, MAMMA1000652, MAMMA1000810, THYRO1001242, MAMMA1001066, MAMMA1002224, MAMMA1001634, MAMMA1001094, MAMMA1002205, NT2RM1000855, NT2RM1000858, Y79AA1002376, NT2RM2000423.

[0211] Thus, characteristic features in the expression of a gene are illustrated by comparing and statistically analyzing the expression of many genes.

Analysis of disease-associated genes

[0212] Non-enzymic protein glycation reaction is believed to be a cause of a variety of chronic diabetic complications. Accordingly, genes of which expression is elevated or decreased in a glycated protein-specific manner in the endothelial cells are associated with diabetic complications caused by glycated proteins. Vascular endothelial cells are affected with glycated proteins present in blood. Reaction products of non-enzymic protein glycation include amadori compound (glycated protein) as a mildly glycated protein and advanced glycation endproduct as a heavily glycated protein. Hence, a survey was carried out for genes of which expression levels are varied depending on the presence of these glycated proteins in endothelial cells. The mRNAs were extracted from endothelial cells that were cultured in the presence or absence of glycated protein. The mRNAs were converted into radiolabeled first strand cDNAs for preparing probes. The probes were hybridized to the above-mentioned DNA array. Signal of each DNA spot was detected by BAS2000 and analyzed by ArrayGauge (Fuji Photo Film Co., Ltd.).

[0213] Advanced glycation endproduct of bovine serum albumin was prepared as follows: bovine serum albumin (BSA; Sigma) was incubated in a phosphate buffer solution containing 50 mM glucose at 37 for 8 weeks; and the resulting brownish BSA was dialyzed against a phosphate buffer solution.

[0214] Human normal pulmonary arterial endothelial cells (Cell Applications) were cultured in an Endothelial Cell Growth Medium (Cell Applications). The culture dish (Farcon) with the cells were incubated in a CO_2 incubator (37., 5% CO_2, in a humid atmosphere). When the cells were grown to be confluent in the dish, 250.g/ml of bovine serum albumin (sigma), glycated bovine serum albumin (Sigma) or advanced glycation endproduct of bovine serum albumin was added thereto and the cells were incubated for 33 hours. The mRNA was extracted from the cells by using a FastTack(TM) 2.0 kit (Invitrogen). The labeling of hybridization probe was carried out by using the mRNA according to the same procedure as described above.

[0215] Table 185 shows the expression level of each cDNA in human pulmonary arterial endothelial cells cultured in a medium containing bovine serum albumin (sigma), glycated bovine serum albumin (Sigma) or advanced glycation endproduct of bovine serum albumin. Genes of which expression was detected in the endothelial cell are as follows: BNGH41000020, BNGH41000087, HEMBA1000275, HEMBA1000300, HEMBA1000477, HEMBA1000634, HEMBA1000671, HEMBA1000713, HEMBA1000745, HEMBA1000835, HEMBA1000875, HEMBA1000940, HEMBA1001390, HEMBA1002131, HEMBA1002163, HEMBA1002164, HEMBA1002195, HEMBA1002227, HEMBA1002239, HEMBA1002420, HEMBA1002767, HEMBA1002992, HEMBA1003047, HEMBA1003120, HEMBA1003294, HEMBA1003315, HEMBA1003602, HEMBA1003945, HEMBA1004007, HEMBA1004067,

HEMBA1004971, HEMBA1005145, HEMBA1005267, HEMBA1005337, HEMBA1005698, HEMBA1005929, HEMBA1005945, HEMBA1006171, HEMBA1006299, HEMBA1006335, HEMBA1006357, HEMBA1006430, HEMBA1006482, HEMBA1006658, HEMBA1006724, HEMBA1006770, HEMBA1006912, HEMBA1006960, HEMBA1007063, HEMBB1000447, HEMBB1000642, HEMBB1000905, HEMBB1001026, HEMBB1001048, HEMBB1001573, HEMBB1001847, HEMBB1001978, HEMBB1002041, HEMBB1002427, HEMBB1002663, HEMBB1002693, MAMMA1000102, MAMMA1000106, MAMMA1000204, MAMMA1000403, MAMMA1000449, MAMMA1000614, MAMMA1000652, MAMMA1000810, MAMMA1000814, MAMMA1000881, MAMMA1000986, MAMMA1001066, MAMMA1001237, MAMMA1001284, MAMMA1001344, MAMMA1001615, MAMMA1001634, MAMMA1001893, MAMMA1001901, MAMMA1001957, MAMMA1002087, MAMMA1002095, MAMMA1002165, MAMMA1002205, MAMMA1002224, MAMMA1002633, MAMMA1003126, NT2RM1000462, NT2RM1000580, NT2RM1000789, NT2RM1000855, NT2RM1000858, NT2RM2000241, NT2RM2000306, NT2RM2000410, NT2RM2000423, NT2RM2000582, NT2RM2000589, NT2RM2000622, NT2RM2000773, NT2RM4000100, NT2RM4000198, NT2RM4000284, NT2RM4000444, NT2RM4000587, NT2RM4000593, NT2RM4000761, NT2RM4000997, NT2RM4001321, NT2RM4001325, NT2RM4001377, NT2RM4001735, NT2RM4001768, NT2RM4001843, NT2RP1000002, NT2RP1000181, NT2RP1000271, NT2RP1000300, NT2RP1000325, NT2RP1000465, NT2RP1000740, NT2RP1000981, NT2RP2000092, NT2RP2000240, NT2RP2000479, NT2RP2000533, NT2RP2000610, NT2RP2000616, NT2RP2000649, NT2RP2000663, NT2RP2000712, NT2RP2000903, NT2RP2001276, NT2RP2001388, NT2RP2001480, NT2RP2001495, NT2RP2001529, NT2RP2001538, NT2RP2001662, NT2RP2001878, NT2RP2001903, NT2RP2001948, NT2RP2001956, NT2RP2002015, NT2RP2002188, NT2RP2002232, NT2RP2002409, NT2RP2002510, NT2RP2002527, NT2RP2002533, NT2RP2002564, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002976, NT2RP2003138, NT2RP2003210, NT2RP2003390, NT2RP2003593, NT2RP2003599, NT2RP2003664, NT2RP2003931, NT2RP2003940, NT2RP2004069, NT2RP2004108, NT2RP2004179, NT2RP2004205, NT2RP2004495, NT2RP2004524, NT2RP2004556, NT2RP2004606, NT2RP2004648, NT2RP2004794, NT2RP2004837, NT2RP2004847, NT2RP2005027, NT2RP2005069, NT2RP2005163, NT2RP2005247, NT2RP2005378, NT2RP2005425, NT2RP2005535, NT2RP2005541, NT2RP2005632, NT2RP2005774, NT2RP2005878, NT2RP2006099, NT2RP2006134, NT2RP2006269, NT2RP2006512, NT2RP3000011, NT2RP3000171, NT2RP3000201, NT2RP3000232, NT2RP3000436, NT2RP3000460, NT2RP3000645, NT2RP3000652, NT2RP3000676, NT2RP3000721, NT2RP3000818, NT2RP3000820, NT2RP3000838, NT2RP3000907, NT2RP3001159, NT2RP3001195, NT2RP3001240, NT2RP3001271, NT2RP3001388, NT2RP3001592, NT2RP3001738, NT2RP3001754, NT2RP3002015, NT2RP3002324, NT2RP3002342, NT2RP3002353, NT2RP3002409, NT2RP3002448, NT2RP3002721, NT2RP3002737, NT2RP3002738, NT2RP3002836, NT2RP3002900, NT2RP3003076, NT2RP3003354, NT2RP3003448, NT2RP3003473, NT2RP3003532, NT2RP3003614, NT2RP3003939, NT2RP3003963, NT2RP3004025, NT2RP3004067, NT2RP3004075, NT2RP3004083, NT2RP3004090, NT2RP3004119, NT2RP3004130, NT2RP3004133, NT2RP3004294, NT2RP3004309, NT2RP3004345, NT2RP3004374, NT2RP3004557, NT2RP3004625, NT2RP3004640, NT2RP3004647, NT2RP4000108, NT2RP4000634, NT2RP4001001, NT2RP4001009, NT2RP4001467, NT2RP4001877, NT2RP4001879, NT2RP4002187, NT2RP4002451, NT2RP4002715, OVARC1000003, OVARC1000090, OVARC1000105, OVARC1000137, OVARC1000208, OVARC1000298, OVARC1000313, OVARC1000331, OVARC1000410, OVARC1000439, OVARC1000553, OVARC1000775, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000956, OVARC1000995, OVARC1001030, OVARC1001049, OVARC1001086, OVARC1001132, OVARC1001222, OVARC1001260, OVARC1001336, OVARC1001569, OVARC1001570, OVARC1001596, OVARC1001607, OVARC1001807, OVARC1001991, PLACE1000231, PLACE1000258, PLACE1000442, PLACE1000740, PLACE1000927, PLACE1001016, PLACE1001100, PLACE1001114, PLACE1001123, PLACE1001229, PLACE1001340, PLACE1001407, PLACE1001464, PLACE1001788, PLACE1001795, PLACE1001918, PLACE1002080, PLACE1002095, PLACE1002329, PLACE1002374, PLACE1002518, PLACE1002547, PLACE1002726, PLACE1002905, PLACE1002911, PLACE1002967, PLACE1003163, PLACE1003407, PLACE1003460, PLACE1003573, PLACE1003598, PLACE1003644, PLACE1003772, PLACE1003839, PLACE1003845, PLACE1004078, PLACE1004166, PLACE1004168, PLACE1004199, PLACE1004279, PLACE1004282, PLACE1004441, PLACE1004482, PLACE1004492, PLACE1004637, PLACE1004887, PLACE1005003, PLACE1005005, PLACE1005031, PLACE1005250, PLACE1005410, PLACE1005519, PLACE1005544, PLACE1005660, PLACE1005669, PLACE1005725, PLACE1005736, PLACE1005745, PLACE1005768, PLACE1005815, PLACE1006073, PLACE1006208, PLACE1006219, PLACE1006290, PLACE1006443, PLACE1006809, PLACE1006959, PLACE1007028, PLACE1007296, PLACE1007626, PLACE1007702, PLACE1007845, PLACE1008282, PLACE1008469, PLACE1008657, PLACE1009196, PLACE1009600, PLACE1003735, PLACE1010081, PLACE1010251, PLACE1010713,

PLACE1011116, PLACE1011181,
PLACE1011236, PLACE1011516, PLACE1011708, PLACE1011824, PLACE1011978, PLACE2000118, PLACE3000181, SKNMC1000004, SKNMC1000014, THYRO1000584, THYRO1000866, THYRO1001113, THYRO1001128, THYRO1001205, THYRO1001242, THYRO1001495, THYRO1001523, THYRO1001529, THYRO1001593, THYRO1001608, THYRO1001702, THYRO1001725, THYRO1001770, THYRO1001803, Y79AA1000117, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1000426, Y79AA1000777, Y79AA1000876, Y79AA1000888, Y79AA1000959, Y79AA1001013, Y79AA1001056, Y79AA1001090, Y79AA1001264, Y79AA1001272, Y79AA1001328, Y79AA1001427, Y79AA1001430, Y79AA1001530, Y79AA1001592, Y79AA1001727, Y79AA1001793, Y79AA1001799, Y79AA1001863, Y79AA1002022, Y79AA1002213, Y79AA1002373, Y79AA1002376, Y79AA1002381.

[0216] Signal ratios of EC_AGE_BSA to EC_BSA and of EC_glycated_BSA to EC_BSA were calculated for each gene. Genes with high signal ratios were selected. In the case of calculating the ratio of signal value of 40 or less to that of more than 40, such signal values were, for convenience, taken as 40 instead of the real values. When the ratio EC_AGE_BSA/EC_BSA is 2 or more, expression of the genes exhibiting such ratio is expected to be elevated due to advanced glycation endproduct of bovine serum albumin. The higher the value is, the higher the gene expression level is. When the ratio EC_AGE_BSA/EC_BSA ranges from 0.5 to 2, expression of the genes exhibiting such ratio is expected to be unaffected due to advanced glycation endproduct of bovine serum albumin. When the ratio EC_AGE_BSA/EC_BSA is less than 0.5, expression of the genes exhibiting such ratio value is expected to be decreased due to advanced glycation endproduct of bovine serum albumin. The lower the value is, the lower the gene expression level is.

[0217] Clone with EC_AGE_BSA/BC_BSA ratio of 2 or higher are as follows: NT2RP2001538, NT2RP4001001 and Y79AA1000967.

[0218] These cDNAs are associated with diabetes.

Analysis of genes associated with neural cell differentiation

[0219] Genes involved in neural cell differentiation are useful for treating neurological diseases. It is possible that genes with varying expression levels in response to induction of cellular differentiation in neural cells are associated with neurological diseases.

[0220] A survey was performed for genes of which expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA)) in cultured cells of a neural strain, NT2.

[0221] The NT2 cells were treated basically according to supplier's instruction manual. "Undifferentiated NT2 cells" means NT2 cells successively cultured in an Opti-MEM I (GIBCO-BRL; catalog No. 31985) containing 10%(v/v) fetal bovine serum and 1%(v/v) penicillin-streptomycin (GIBCO BRL). "NT2 cells cultured in the presence of retinoic acid" means the cells resulted from transferring undifferentiated NT2 cells into a retinoic acid-containing medium, which consists of D-MEM (GIBCO BRL; catalog No. 11965), 10%(v/v) fetal bovine serum, 1%(v/v) penicillin-streptomycin and 10 M retinoic acid (GIBCO-BRL), and the subsequent successive culture therein for 5 weeks. "NT2 cells that were cultured in the presence of retinoic acid and then further cultured in the presence of cell-division inhibitor added" means NT2 cells resulted from transferring NT2 cells cultured in the presence of retinoic acid for 5 weeks into a cell-division inhibitor-containing medium, which consisted of D-MEM(GIBCO BRL; catalog No.11965), 10%(v/v) fetal bovine serum, 1%(v/v) penicillin-streptomycin, 10. M retinoic acid, 10.M FudR (5-fluoro-2'-deoxyuridine: GIBCO BRL), 10. M Urd (Uridine: GIBCO BRL) and 1.M araC (Cytosine.-D-Arabinofuranoside: GIBCO BRL), and the subsequence successive culture for 2 weeks. Each of the cells were treated with trypsin and then harvested. Total RNAs were extracted from the cells by using S.N.A.P.(TM) Total RNA Isolation kit (Invitrogen). The labeling of probe used for hybridization was carried out by using 10.g of the total RNA according to the same methods as described above. The data were obtained in triplicate (n=3). The data of signal value representing gene expression level in the cells in the presence of stimulation for inducing differentiation were compared with those in the absence of the stimulation. The comparison was performed by statistical treatment of two-sample t-test. Clones with significant difference in the signal distribution were selected under the condition of $p<0.05$. In this analysis, clones with the difference can be statistically detected even when the signals were low. Accordingly, clones with signal value of 40 or less were also assessed for the selection.

[0222] Tables 186-365 show the expression level of each cDNA in undifferentiated NT2 cells, NT2 cells cultured in the presence of RA, and NT2 cells that were cultured in the presence of RA and that were further cultured in the presence of cell-division inhibitor added.

[0223] Averaged signal values (M_1, M_2) and sample variances (s_1^2, s_2^2) were calculated for each gene in each of the cells, and then, the pooled sample variances s^2 were obtained from the sample variances of the two types of cells to be compared. The t values were determined according to the following formula: $t=(M1-M2)/s/(1/3+1/3)^{1/2}$. When the determined t-value was greater than a t-value at P, which means the probability of significance level, of 0.05 or 0.01 in the t-distribution table with 4 degrees of freedom, the difference was judged to be found in the expression level of the gene between the two types of cells at $p<0.05$ or $p<0.01$, respectively. The tables also include the information on

an increase (+) or decrease (-) in the expression level of a gene in the treated cells when the level is compared with that of untreated undifferentiated cells.

[0224] Clones of which expression levels increased by RA are as follows: HEMBA1000121, HEMBA1000275, HEMBA1000300, HEMBA1000634, HEMBA1000671, HEMBA1000875, HEMBA1001184, HEMBA1001390, HEMBA1001886, HEMBA1002163, HEMBA1002227, HEMBA1002420, HEMBA1002421, HEMBA1003072, HEMBA1003120, HEMBA1003294, HEMBA1003497, HEMBA1004007, HEMBA1004110, HEMBA1004391, HEMBA1004444, HEMBA1005230, HEMBA1005246, HEMBA1005267, HEMBA1005489, HEMBA1005913, HEMBA1006299, HEMBA1006357, HEMBA1006517, HEMBA1006544, HEMBA1006658, HEMBA1006749, HEMBA1007063, HEMBA1007241, HEMBB1000447, HEMBB1000542, HEMBB1000567, HEMBB1000642, HEMBB1000668, HEMBB1001026, HEMBB1001847, HEMBB1002051, HEMBB1002120, HEMBB1002228, HEMBB1002693, MAMMA1000106, MAMMA1000141, MAMMA1000473, MAMMA1000528, MAMMA1000810, MAMMA1000881, MAMMA1001634, MAMMA1001957, MAMMA1002205, MAMMA1002224, NT2RM2000423, NT2RM2000497, NT2RM2000582, NT2RM2001126, NT2RM2001902, NT2RM4000198, NT2RM4000284, NT2RM4000593, NT2RM4001321, NT2RP1000002, NT2RP1000050, NT2RP1000181, NT2RP1000261, NT2RP1000465, NT2RP1000468, NT2RP1000579, NT2RP1000679, NT2RP2000092, NT2RP2000479, NT2RP2000610, NT2RP2000663, NT2RP2000694, NT2RP2000903, NT2RP2001388, NT2RP2001538, NT2RP2001878, NT2RP2001015, NT2RP2002304, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002974, NT2RP2002976, NT2RP2003179, NT2RP2003302, NT2RP2003383, NT2RP2003469, NT2RP2003664, NT2RP2003940, NT2RP2004069, NT2RP2004108, NT2RP2004524, NT2RP2004556, NT2RP2004670, NT2RP2005069, NT2RP2005247, NT2RP2005425, NT2RP2005463, NT2RP2005514, NT2RP2005535, NT2RP2005541, NT2RP2005774, NT2RP2005878, NT2RP2005883, NT2RP2005887, NT2RP2006099, NT2RP2006134, NT2RP3000011, NT2RP3000125, NT2RP3000171, NT2RP3000232, NT2RP3000460, NT2RP3000481, NT2RP3000652, NT2RP3000677, NT2RP3000818, NT2RP3000820, NT2RP3001044, NT2RP3001061, NT2RP3001170, NT2RP3001240, NT2RP3001322, NT2RP3001388, NT2RP3001542, NT2RP3001592, NT2RP3001976, NT2RP3002790, NT2RP3002900, NT2RP3002983, NT2RP3003000, NT2RP3003354, NT2RP3003532, NT2RP3003729, NT2RP3003874, NT2RP3003939, NT2RP3004025, NT2RP3004083, NT2RP3004090, NT2RP3004130, NT2RP3004202, NT2RP3004294, NT2RP3004640, NT2RP4000108, NT2RP4000634, NT2RP4002451, NT2RP4002715, OVARC1000090, OVARC1000208, OVARC1000275, OVARC1000553, OVARC1000775, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000995, OVARC1001030, OVARC1001049, OVARC1001132, OVARC1001596, OVARC1002178, PLACE1000258, PLACE1000442, PLACE1000927, FLACE1000986, PLACE1001100, PLACE1001123, PLACE1001795, PLACE1002518, PLACE1002547, PLACE1002967, PLACE1003407, PLACE1003428, PLACE1003644, PLACE1003839, PLACE1004078, PLACE1004441, PLACE1004450, PLACE1005669, PLACE1005682, PLACE1005736, PLACE1005768, PLACE1005815, PLACE1006073, PLACE1006208, PLACE1007296, PLACE1007626, PLACE1008282, PLACE1008984, PLACE1008985, PLACE1010445, PLACE1011708, PLACE1011978, PLACE4000455, SKNMC1000004, THYRO1000036, THYRO1000580, THYRO1000776, THYRO1000999, THYRO1001063, THYRO1001128, THYRO1001205, THYRO1001327, THYRO1001523, THYRO1001725, THYRO1001770, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1001056, Y79AA1001062, Y79AA1001090, Y79AA1001727, Y79AA1002213, Y79AA1002381.

[0225] Clones of which expression levels decreased by RA are as follows: BNGH41000020, HEMBA1005070, NT2RP2005027, NT2RP3003473, Y79AA1002376.

[0226] Clones of which expression levels increase by RA/inhibitor are as follows:

HEMBA1000128, HEMBA1000875, HEMBA1001390, HEMBA1002163, HEMBA1002227, HEMBA1002421, HEMBA1004391, HEMBA1004454, HEMBA1004785, HEMBA1005913, HEMBA1006171, HEMBA1006299, HEMBA1006335, HEMBA1006544, HEMBA1007241, HEMBB1000447, HEMBB1000668, MAMMA1000994, MAMMA1001344, NT2RM2000582, NT2RP1001004, NT2RP2000663, NT2RP2000694, NT2RP2000903, NT2RP2001388, NT2RP2002674, NT2RP2002974, NT2RP2003383, NT2RP2004069, NT2RP2004606, NT2RP2004837, NT2RP2005069, NT2RP2005425, NT2RP2005463, NT2RP2005541, NT2RP2005883, NT2RP2005887, NT2RP3000460, NT2RP3000838, NT2RP3001044, NT2RP3001240, NT2RP3001388, NT2RP3002721, NT2RP3002738, NT2RP3003469, NT2RP3004083, NT2RP3004130, NT2RP3004202, NT2RP3004294, NT2RP3004640, NT2RP4000108, NT2RP4002451, NT2RP4002715, OVARC1000275, OVARC1000467, OVARC1000553, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000995, OVARC1001030, OVARC1001222, OVARC1001596, OVARC1002058, OVARC1002178, PLACE1000927, PLACE1001123, PLACE1001407, PLACE1001464, PLACE1001564, PLACE1001795, PLACE1002547, PLACE1003407, PLACE1003644, PLACE1003845, PLACE1004441, PLACE1004482, PLACE1005410, PLACE1005601, PLACE1005725, PLACE1005736, PLACE1006093, PLACE1006219, PLACE1006290, PLACE1006716, PLACE1007296, PLACE1007626, PLACE1008359, PLACE1010968, PLACE1011364,

PLACE1011824, THYRO1000678, THYRO1000776, THYRO1000999, THYRO1001113, THYRO1001237, THYRO1001523, Y79AA1000226, Y79AA1000888, Y79AA1001430.

[0227] Clones of which expression levels decrease by RA/inhibitor are as follows: HEMBA1000349, HEMBA1001297, HEMBA1001878, HEMBA1005070, HEMBA1006482, HEMBB1001959, NT2RM2001939, NT2RP1000981, NT2RP2001469, NT2RP3003473, OVARC1001132, PLACE1001655, Y79AA1000127, Y79AA1002381.

[0228] Clones of which expression levels increase in the presence of both RA and RA/inhibitor are as follows: HEMBA1000875, HEMBA1001390, HEMBA1002163, HEMBA1002227, HEMBA1002421, HEMBA1004391, HEMBA1005913, HEMBA1006299, HEMBA1006544, HEMBA1007241, HEMBB1000447, HEMBB1000668, NT2RM2000582, NT2RP2000663, NT2RP2000694, NT2RP2000903, NT2RP2001388, NT2RP2002974, NT2RP2003383, NT2RP2004069, NT2RP2005069, NT2RP2005425, NT2RP2005463, NT2RP2005541, NT2RP2005883, NT2RP2005887, NT2RP3000460, NT2RP3001044, NT2RP3001240, NT2RP3001388, N12RP3004083, NT2RP3004130, NT2RP3004202, NT2RP3004294, NT2RP3004640, NT2RP4000108, NT2RP4002451, NT2RP4002715, OVARC1000275, OVARC1000553, OVARC1000853, OVARC1000873, OVARC1000916, OVARC1000995, OVARC1001030, OVARC1001596, OVARC1002178, PLACE1000927, PLACE1001123, PLACE1001795, PLACE1002547, PLACE1003407, PLACE1003644, PLACE1004441, PLACE1005736, PLACE1007296, PLACE1007626, THYRO1000776, THYRO1000999, THYRO1001523, Y79AA1000226.

[0229] Clones of which expression levels decrease in the presence of both RA and RA/inhibitor are as follows: HEMBA1005070 and NT2RP3003473.

[0230] These are neurological disease-associated clones.

Analysis of rheumatoid arthritis-associated genes

[0231] The onset of rheumatoid arthritis is thought to be involved in the proliferation of synovial cells covering inner surfaces of joint cavity and in inflammatory reaction resulted from the action of cytokines produced by leukocytes infiltrating into the joint synovial tissues (Rheumatism Information Center.http://www.rheuma-net.or.jp/). Recent studies have also revealed that tissue necrosis factor (TNF)-. participates in the onset (Current opinion in immunology 1999, 11, 657-662). When the expression of a gene exhibits responsiveness to the action of TNF on synovial cells, the gene is considered to be involved in rheumatoid arthritis.

[0232] A survey was performed for genes of which expression levels are varied in response to TNF-. in the primary cell culture of synovial tissue. The primary cultured cells of the smooth muscle (Cell Applications) were grown to be confluent in a culture dish, and then, human TNF-. (Boehringer-Mannheim) was added at a final concentration of 10 ng/ml thereto. The culture was further continued for 24 hours.

[0233] Total RNA was extracted from the cells by using S.N.A.P.(TM) Total RNA Isolation kit (Invitrogen). The labeling of probe used for hybridization was carried out by using 10.g of the total RNA according to the same methods as described above. The data were obtained in tripricate (n=3). The data of signal value representing gene expression level in the cells in the presence of TNF stimulation were compared with those in the absence of the stimulation. The comparison was performed by statistical treatment of two-sample t-test. Clones with significant difference in the signal distribution were selected under the condition of $p<0.05$. In this analysis, clones with the difference can be statistically detected even when the signals were low. Accordingly, clones with signal value of 40 or less were also assessed for the selection.

[0234] Table 366 shows the expression level of each cDNA in synovial cells cultured in the absence or presence of TNF.

[0235] Averaged signal values (M_1, M_2) and sample variances (s_1^2, s_2^2) for each gene were calculated in each of the cells, and then, the pooled sample variances s^2 were obtained from the sample variances of the two types of cells to be compared. The t-values were determined according to the following formula: $t=(M_1-M_2)/s/(1/3+1/3)^{1/2}$. When the determined t-value was greater than a t-value at P, which means the probability of significance level, of 0.05 or 0.01 in the t-distribution table with 4 degrees of freedom, the difference was judged to be found in the expression level of the gene between the two types of cells at $p<0.05$ or $p<0.01$, respectively. The tables also include the information of an increase (+) or decrease (-) in the expression level of a gene in the stimulated cells when the level is compared with that of unstimulated cells.

[0236] Clones of which expression levels are elevated by TNF-. are as follows: BNGH41000020, HEMBA1000349, HEMBA1000634, HEMBA1000671, HEMBA1000835, HEMBA1000962, HEMBA1002178, HEMBA1002195, HEMBA1002239, HEMBA1002420, HEMBA1002524, HEMBA1002992, HEMBA1003315, HEMBA1003392, HEMBA1003487, HEMBA1003602, HEMBA1004067, HEMBA1004797, HEMBA1005337, HEMBA1005489, HEMBA1006916, HEMBB1000668, HEMBB1000905, HEMBB1001547, HEMBB1001573, HEMBB1002041, HEMBB1002663, MAMMA1000652, MAMMA1000810, MAMMA1001634,

MAMMA1002091, MAMMA1002234, NT2RM2000306, NT2RM4000417, NT2RP1000002, NT2RP1000181, NT2RP1000740, NT2RP2000694, NT2RP2001921, NT2RP2002527, NT2RP2004495, NT2RP2004606, NT2RP2005163, NT2RP2005463, NT2RP2006134, NT2RP3000171, NT2RP3000652, NT2RP3001195, NT2RP3001976, NT2RP3003473, NT2RP3003874, NT2RP3004090, NT2RP3004294, NT2RP3004557, NT2RP3004647, NT2RP4000108, NT2RP4001001, NT2RP4001877, OVARC1000090, OVARC1000105, OVARC1000275, OVARC1000439, OVARC1001607, PLACE1000740, PLACE1000927, PLACE1001016, PLACE1001100, PLACE1001464, PLACE1001500, PLACE1001918, PLACE1002095, PLACE1002547, PLACE1003644, PLACE1004519, PLACE1005031, PLACE1005410, PLACE1005736, PLACE1006219, PLACE1006809, PLACE1008716, PLACE1010081, THYRO1001770, Y79AA1000127, Y79AA1000207, Y79AA1000270, Y79AA1000876, Y79AA1001013, Y79AA1001264, Y79AA1001272, Y79AA1001328, Y79AA1001430, Y79AA1001530, Y79AA1001799.

[0237] Clones of which expression levels decrease by TNF-. are as follows: NT2RM4000326, NT2RP1000300, NT2RP2000514, NT2RP2001755, NT2RP2006042, NT2RP3000481, NT2RP3002790. These are rheumatoid arthritis-associated clones.

EXAMPLE 16

Search for a signal sequence, transmembrane region and functional domain in deduced amino acid sequences

[0238] The deduced amino acid sequences from the full-length nucleotide sequences were examined to predict the presence of a signal sequence in their amino-termini as well as the presence of a transmembrane region. The amino acid sequences were also searched for a protein functional domain (motif). The examinations for a signal sequence in the amino-terminus, for a transmembrane region and for a functional domain were performed by using PSORT [K. Nakai & M. Kanehisa, Genomics, 14:897-911 (1992)], SOSUI [T. Hirokawa et al., Bioinformatics, 14:378-379 (1998)] (Mitsui Knowledge Industry Co., Ltd.) and Pfam (http://www.sanger.ac.uk/Software/Pfam/index.shtml), respectively. When the presence of a signal sequence or a transmembrane region in the amino-terminus was predicted in the amino acid sequence by PSORT or SOSUI, the protein was predicted to be a secretory protein or a transmembrane protein. When the amino acid sequence matched a functional domain in the Pfam search for a functional domain, the function of the protein is predictable based on the matching data, for example, by referring to the functional categories in PROSITE (http://www.expasy.ch/cgi-bin/prosite-list.pl). The functional domain search can be performed by using PROSITE instead of Pfam.

[0239] Search results obtained by using the respective software programs are indicated below.

[0240] Clones whose deduced amino acid sequences were predicted to have signal sequences by PSORT search are as follows:

HEMBA1000713, HEMBA1002420, HEMBA1002421, HEMBA1003101, HEMBA1004110, HEMBA1006707, HEMBA1006902, HEMBB1001530, HEMBB1001573, HEMBB1001978, HEMBB1002162, HEMBB1002245, HEMBB1002427, MAMMA1000102, MAMMA1000118, MAMMA1000457, MAMMA1001043, MAMMA1001344, MAMMA1001893, MAMMA1002070, MAMMA1002165, MAMMA1002633, NT2RM2000241, NT2RM2000410, NT2RM2001941, NT2RM4001325, NT2RP1001563, NT2RP2001495, NT2RP2002063, NT2RP2002721, NT2RP2003383, NT2RP2003593, NT2RP2003655, NT2RP2003664, NT2RP2004179, NT2RP2004205, NT2RP2004524, NT2RP2005463, NT2RP3000460, NT2RP3001012, NT2RP3001858, NT2RP3002836, NT2RP3003076, NT2RP3003532, NT2RP3004133, NT2RP3004309, NT2RP4001467, NT2RP4002451, OVARC1000298, OVARC1000811, PLACE1000231, PLACE1000740, PLACE1001183, PLACE1001536, PLACE1001564, PLACE1002095, PLACE1002374, PLACE1003839, PLACE1001482, PLACE1005005, PLACE1005250, PLACE1005383, PLACE1005410, PLACE1005544, PLACE1005569, PLACE1006093, PLACE1006277, PLACE1006809, PLACE1007626, PLACE1008359, PLACE1009067, PLACE1010251, PLACE1011236, SKNMC1000004, SKNMC1000014, THYRO1000099, THYRO1000196, THYRO1001237, THYRO1001327, THYRO1001523, THYRO1001702, THYRO1001725, Y79AA1000426, Y79AA1000521, Y79AA1000959, Y79AA1001013, Y79AA1001264, Y79AA1001328, Y79AA1001427, Y79AA1001430, Y79AA1001795, Y79AA1001803, Y79AA1002022,

[0241] Clones whose deduced amino acid sequences were predicted to have transmembrane regions by SOSUI search are as follows: BNGH41000091, HEMBA1000121, HEMBA1000349, HEMBA1000477, HEMBA1000713, HEMBA1000940, HEMBA1000962, HEMBA1001221, HEMBA1001228, HEMBA1001621, HEMBA1002167, HEMBA1002195, HEMBA1002227, HEMBA1002421, HEMBA1003101, HEMBA1003392, HEMBA1003530, HEMBA1003732, HEMBA1003945, HEMBA1004391, HEMBA1004454, HEMBA1004797, HEMBA1004982, HEMBA1005449, HEMBA1005522, HEMBA1005545, HEMBA1005698, HEMBA1006171, HEMBA1006299, HEMBA1006311, HEMBA1006335, HEMBA1006357, HEMBA1006430, HEMBA1006724, HEMBA1006960, HEMBB1000407, HEMBB1000447, HEMBB1000567, HEMBB1000679, HEMBB1000905, HEMBB1001026,

HEMBB1001407, HEMBB1001573, HEMBB1001978, HEMBB1002041, HEMBB1002162, HEMBB1002245, HEMBB1002427, HEMBB1002693, MAMMA1000102, MAMMA1000106, MAMMA1000118, MAMMA1000141, MAMMA1000204, MAMMA1000226, MAMMA1000457, MAMMA1000473, MAMMA1000591, MAMMA1000681, MAMMA1000810, MAMMA1000986, MAMMA1001043, MAMMA1001141, MAMMA1001237, MAMMA1001344, MAMMA1001893, MAMMA1001957, MAMMA1001978, MAMMA1002070, MAMMA1002091, MAMMA1002095, MAMMA1002633, NT2RM1000580, NT2RM1000855, NT2RM1000858, NT2RM2000410, NT2RM2000565, NT2RM2001626, NT2RM2001939, NT2RM2001941, NT2RM4000444, NT2RM4000587, NT2RM4000648, NT2RM4000997, NT2RM4001325, NT2RM4001735, NT2RM4001768, NT2RM4002352, NT2RP1000050, NT2RP1000181, NT2RP1000261, NT2RP1000300, NT2RP1000448, NT2RP1000551, NT2RP1000613, NT2RP1000981, NT2RP1001563, NT2RP2000479, NT2RP2000533, NT2RP2000649, NT2RP2000663, NT2RP2000694, NT2RP2000818, NT2RP2000903, NT2RP2001200, NT2RP2001276, NT2RP2001495, NT2RP2001915, NT2RP2001956, NT2RP2002188, NT2RP2002232, NT2RP2002527, NT2RP2002533, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002976, NT2RP2003042, NT2RP2003390, NT2RP2003469, NT2RP2003593, NT2RP2003655, NT2RP2003664, NT2RP2003950, NT2RP2004179, NT2RP2004205, NT2RP2004495, NT2RP2004524, NT2RP2004556, NT2RP2004606, NT2RP2004648, NT2RP2004794, NT2RP2005163, NT2RP2005181, NT2RP2005463, NT2RP2005597, NT2RP2005666, NT2RP2005883, NT2RP2005994, NT2RP2006004, NT2RP2006269, NT2RP2006512, NT2RP2006580, NT2RP3000169, NT2RP3000171, NT2RP3000304, NT2RP3000460, NT2RP3000616, NT2RP3000721, NT2RP3000818, NT2RP3000907, NT2RP3000921, NT2RP3001159, NT2RP3001195, NT2RP3001240, NT2RP3001271, NT2RP3001322, NT2RP3001388, NT2RP3001560, NT2RP3001592, NT2RP3001650, NT2RP3001738, NT2RP3002015, NT2RP3002311, NT2RP3002342, NT2RP3002411, NT2RP3002790, NT2RP3002836, NT2RP3002900, NT2RP3002958, NT2RP3003000, NT2RP3003354, NT2FP3003532, NT2RP3003535, NT2RP3003614, NT2RP3004025, NT2RP3004075, NT2RP3004083, NT2RP3004090, NT2RP3004130, NT2RP3004294, NT2RP3004309, NT2RP3004345, NT2RP3004406, NT2RP3004481, NT2RP3004552, NT2RP4001001, NT2RP4001009, NT2RP4001467, NT2RP4001879, NT2RP4002187, NT2RP4002451, NT2RP4002750, OVARC1000003, OVARC1000105, OVARC1000307, OVARC1000439, OVARC1000553, OVARC1001030, OVARC1001336, OVARC1001570, PLACE1000231, PLACE1000560, PLACE1000740, PLACE1000912, PLACE1000914, PLACE1000927, PLACE1001016, PLACE1001183, PLACE1001231, PLACE1001401, PLACE1001407, PLACE1001464, PLACE1001536, PLACE1001564, PLACE1001655, PLACE1001836, PLACE1001918, PLACE1001949, PLACE1002518, PLACE1002726, PLACE1002967, PLACE1003573, PLACE1003737, PLACE1003839, PLACE1003845, PLACE1003852, PLACE1004279, PLACE1004282, PLACE1004441, PLACE1004637, PLACE1004648, PLACE1004816, PLACE1004887, PLACE1005003, PLACE1005005, PLACE1005410, PLACE1005544, PLACE1005569, PLACE1005660, PLACE1005725, PLACE1005745, PLACE1005927, PLACE1006290, PLACE1006443, PLACE1006959, PLACE1007096, PLACE1007296, PLACE1007626, PLACE1007881, PLACE1008359, PLACE1008469, PLACE1008716, PLACE1008985, PLACE1009196, PLACE1009279, PLACE1009527, PLACE1009546, PLACE1009600, PLACE1010011, PLACE1010078, PLACE1010445, PLACE1010713, PLACE1010784, PLACE1010968, PLACE1011236, PLACE1011516, PLACE3000181, THYRO1000400, THYRO1000678, THYRO1000776, THYRO1000956, THYRO1001102, THYRO1001113, THYRO1001205, THYRO1001237, THYRO1001242, THYRO1001266, THYRO1001327, THYRO1001478, THYRO1001523, THYRO1001641, THYRO1001702, THYRO1001725, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1000521, Y79AA1000888, Y79AA1001013, Y79AA1001212, Y79AA1001264, Y79AA1001328, Y79AA1001426, Y79AA1001427, Y79AA1001727, Y79AA1001787, Y79AA1001795, Y79AA1001803, Y79AA1002058, Y79AA1002129, Y79AA1002213, Y79AA1002373,

[0242] Names of clones whose deduced amino acid sequences were predicted to have functional domains by Pfam search, and names of the matched functional domains are shown below. When multiple functional domains matched a clone, each domain name was indicated, separated by a double-slash mark,//.

HEMBA1000006//Src homology domain 3
HEMBA1000128//SCP-like extracellular Proteins
HEMBA1000349//ABC transporters
HEMBA1000462//RNA recognition motif. (aka RRM, RBD, or RNP domain)
HEMBA1000590//EGF-like domain//von Willebrand factor type A domain
HEMBA1000671//Zinc finger, C2H2 type
HEMBA1000732//EGF-like domain
HEMBA1000940//Connexin
HEMBA1001221//EGF-like domain//Kazal-type serine protease inhibitor domain

HEMBA1001621//7 transmembrane receptor (rhodopsin family)
HEMBA1001878//WD domain, G-beta repeats
HEMBA1002048//Zinc finger, C2H2 type
HEMBA1002167//Carboxylesterases
HEMBA1002551//WD domain, G-beta repeats
HEMBA1002992//Ubiquitin family
HEMBA1003047//CUB domain
HEMBA1003120//Zinc finger, C2H2 type
HEMBA1003230//EGF-like domain
HEMBA1003392//Low-density lipoprotein receptor domain class A
HEMBA1003497//Zinc finger, C2H2 type
HEMBA1004250//Cadherin
HEMBA1004391//Fibronectin type III domain//IG superfamily
HEMBA1004454//4 transmembrane segments integral membrane proteins
HEMBA1004785//'chromo' (CHRomatin Organization MOdifier) domain
HEMBA1005246//Zinc finger, C2H2 type
HEMBA1005267//Ank repeat
HEMBA1005545//7 transmembrane receptor (rhodopsin family)
HEMBA1005929//Eukaryotic protein kinase domain
HEMBA1005945//Mitochondrial carrier proteins
HEMBA1006572//Zinc finger, C2H2 type
HEMBA1006707//EGF-like domain//von Willebrand factor type A domain
HEMBA1006749//EGF-like domain//von Willebrand factor type A domain
HEMBA1006770//RNA recognition motif. (aka RRM, RBD, or RNP domain)
HEMBA1006902//EGF-like domain//von Willebrand factor type A domain
HEMBB1000106//Zinc finger, CCHC class
HEMBB1000668//WD domain, G-beta repeats
HEMBB1000881//Thrombospondin type 1 domain
HEMBB1000905//WD domain, G-beta repeats
HEMBB1002041//EGF-like domain//Kazal-type serine protease inhibitor domain
HEMBB1002245//IG superfamily
HEMBB1002302//Zinc finger, CCHC class
HEMBB1002465//Acyl-CoA dehydrogenases
HEMBB1002661//Helix-loop-helix DNA-binding domain
MAMMA1000204//C2 domain
MAMMA1000457//FAD/NAD-binding domain in oxidoreductases
MAMMA1000681//7 transmembrane receptor (rhodopsin family)
MAMMA1000881//Eukaryotic protein kinase domain//Protein kinase C terminal domain
MAMMA1001150//Phorbol esters / diacylglycerol binding domain//Eukaryotic protein kinase domain
MAMMA1001310//WD domain, G-beta repeats
MAMMA1001532//Zinc finger, C2H2 type
MAMMA1001615//Helix-loop-helix DNA-binding domain
MAMMA1002070//Kringle domain
MAMMA1002080//Ras family (contains ATP/GTP binding P-loop)
MAMMA1002095//E1-E2 ATPases
MAMMA1002165//Insulin-like growth factor binding proteins
NT2RM1000789//HMG (high mobility group) box
NT2RM1000855//eubacterial secY protein
NT2RM1000899//Mitochondrial carrier proteins
NT2RM2000589//PH (pleckstrin homology) domain
NT2RM2000632//Helicases conserved C-terminal domain
NT2RM2001792//Fibrinogen beta and gamma chains, C-terminal globular domain
NT2RM2001902//Eukaryotic protein kinase domain
NT2RM2001939//7 transmembrane receptor (rhodopsin family)
NT2RM2001941//7 transmembrane receptor (rhodopsin family)
NT2RM4000284//Class I Histocompatibility antigen, domains alpha 1 and 2
NT2RM4000326//Zinc finger, C2H2 type
NT2RM4000417//C2 domain

NT2RM4000444//ABC transporters
NT2RM4001377//PH (pleckstrin homology) domain
NT2RM4001768//Alcohol/other dehydrogenases, short chain type
NT2RM4002352//Low-density lipoprotein receptor domain class A
NT2RP1000181//Heme-binding domain in cytochrome b5 and oxidoreductases
NT2RP1000271//Zinc finger, C2H2 type
NT2RP1000325//Mitochondrial carrier proteins
NT2RP1000613//Eukaryotic-type carbonic anhydrases
NT2RP1000981//IG superfamily
NT2RP1001004//Thrombospondin type 1 domain
NT2RP1001020//Eukaryotic protein kinase domain
NT2RP1001031//WD domain, G-beta repeats
NT2RP1001563//EGF-like domain//Lectin C-type domain short and long forms//SCP-like extracellular Proteins
NT2RP2000092//Zinc finger, C2H2 type
NT2RP2000514//Fibronectin type III domain//IG superfamily
NT2RP2000649//Zinc-binding metalloprotease domain
NT2RP2000712//Zinc finger, C2H2 type
NT2RP2000739//Zinc finger, C2H2 type
NT2RP2001514//E1-E2 ATPases
NT2RP2001529//Eukaryotic protein kinase domain
NT2RP2001755//Thrombospondin type 1 domain
NT2RP2001769//Eukaryotic protein kinase domain
NT2RP2002188//Carboxylesterases
NT2RP2002527//Heme-binding domain in cytochrome b5 and oxidoreductases
NT2RP2002564//Zinc finger, C2H2 type
NT2RP2002942//IG superfamily
NT2RP2003179//Eukaryotic protein kinase domain
NT2RP2003302//Zinc finger, C2H2 type
NT2RP2003390//DnaJ, prokaryotic heat shock protein
NT2RP2003469//Sugar (and other) transporters
NT2RP2003545//Eukaryotic protein kinase domain
NT2RP2003593//Thioredoxins
NT2RP2003940//Zinc finger, C2H2 type
NT2RP2004108//Zinc finger, C2H2 type
NT2RP2004205//IG superfamily
NT2RP2004670//Eukaryotic protein kinase domain
NT2RP2004847//Zinc finger, C2H2 type
NT2RP2005181//Amino acid permeases
NT2RP2005247//Zinc finger, C3HC4 type (RING finger)
NT2RP2005391//Fibronectin type III domain
NT2RP2005535//Zinc finger, C2H2 type
NT2RP2005774//Zinc finger, C2H2 type
NT2RP2005878//Alcohol/other dehydrogenases, short chain type
NT2RP2005941//Homeobox domain//'Paired box' domain
NT2RP2006004//Fibronectin type III domain
NT2RP3000011//WD domain, G-beta repeats
NT2RP3000022//Eukaryotic protein kinase domain
NT2RP3000063//Zinc finger, C2H2 type
NT2RP3000148//Zinc finger, C2H2 type
NT2RP3000172//Eukaryotic protein kinase domain
NT2RP3000201//Eukaryotic protein kinase domain
NT2RP3000232//Zinc finger, C2H2 type
NT2RP3000304//Low-density lipoprotein receptor domain class A//Low-density lipoprotein receptor domain class B
NT2RP3000436//Thioredoxins
NT2RP3000460//eubacterial secY protein
NT2RP3000616//Fibronectin type III domain
NT2RP3000652//Zinc finger, C2H2 type

NT2RP3000676//Mitochondrial carrier proteins
NT2RP3000789//KH domain family of RNA binding proteins
NT2RP3000820//WD domain, G-beta repeats
NT2RP3000838//PH (pleckstrin homology) domain
NT2RP3000907//E1-E2 ATPases
NT2RP3000921//IG superfamily
NT2RP3001195//Sugar (and other) transporters
NT2RP3001240//eubacterial secY protein
NT2RP3001388//C2 domain
NT2RP3001650//CUB domain//Low-density lipoprotein receptor domain class A
NT2RP3001738//Heme-binding domain in cytochrome b5 and oxidoreductases
NT2RP3001976//Zinc finger, C2H2 type
NT2RP3002281//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP3002411//Alcohol/other dehydrogenases, short chain type
NT2RP3002721//Citrate synthase
NT2RP3003000//Ion transport proteins
NT2RP3003527//Eukaryotic protein kinase domain
NT2RP3003535//TPR Domain
NT2RP3003849//C2 domain
NT2RP3004067//Src homology domain 3
NT2RP3004090//Zinc finger, C3HC4 type (RING finger)
NT2RP3004481//IG superfamily
NT2RP3004552//CUB domain//Sushi domain
NT2RP3004647//Mitochondrial carrier proteins
NT2RP4000108//Intermediate filament proteins
NT2RP4000634//Eukaryotic protein kinase domain
NT2RP4000962//Eukaryotic protein kinase domain
NT2RP4001009//Zinc-binding metalloprotease domain
NT2RP4001877//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP4002187//Alcohol/other dehydrogenases, short chain type
NT2RP4002750//Amino acid permeases
OVARC1000105//Ubiquitin-conjugating enzymes
OVARC1000255//Eukaryotic protein kinase domain
OVARC1000313//Thioredoxins
OVARC1000410//Fibrinogen beta and gamma chains, C-terminal globular domain
OVARC1000529//Eukaryotic protein kinase domain
OVARC1000811//CUB domain//Kringle domain
OVARC1000916//Eukaryotic protein kinase domain
OVARC1001049//Helix-loop-helix DNA-binding domain
OVARC1001338//Eukaryotic protein kinase domain
OVARC1001569//Eukaryotic protein kinase domain
OVARC1001570//Eukaryotic aspartyl proteases
PLACE1000231//WAP-type (Whey Acidic Protein) 'four-disulfide core'
PLACE1000258//Zinc finger, C2H2 type
PLACE1000740//EGF-like domain
PLACE1000907//Zinc finger, C2H2 type
PLACE1001016//Ion transport proteins
PLACE1001500//Helicases conserved C-terminal domain
PLACE1001655//Ion transport proteins
PLACE1001795//SCP-like extracellular Proteins
PLACE1001949//E1-E2 ATPases
PLACE1002329//Src homology domain 3
PLACE1002355//Alpha-2-macroglobulin family//Kazal-type serine protease inhibitor domain
PLACE1002374//Cysteine proteases
PLACE1002518//Zinc finger, C3HC4 type (RING finger)
PLACE1002911//IG superfamily
PLACE1003135//Eukaryotic protein kinase domain
PLACE1003163//Enoyl-CoA hydratase/isomerase

PLACE1003573//Lectin C-type domain short and long forms
PLACE1004166//Bromodomain
PLACE1004305//Ras family (contains ATP/GTP binding P-loop)
PLACE1004441//7 transmembrane receptor (rhodopsin family)
PLACE1004520//IG superfamily
PLACE1004816//Fibrinogen beta and gamma chains, C-terminal globular domain
PLACE1004887//Zinc finger, C3HC4 type (RING finger)
PLACE1005003//Trypsin
PLACE1005383//EGF-like domain
PLACE1005410//eubacterial secY protein
PLACE1005426//IG superfamily
PLACE1005519//Eukaryotic protein kinase domain
PLACE1005539//Heat shock hsp20 proteins
PLACE1005544//IG superfamily
PLACE1005569//IG superfamily
PLACE1005682//Zinc finger, C3HC4 type (RING finger)
PLACE1005736//PH (pleckstrin homology) domain
PLACE1006079//Homeobox domain
PLACE1006716//C1q domain
PLACE1008282//Eukaryotic protein kinase domain
PLACE1008549//Ets-domain
PLACE1008744//EGF-like domain//Sushi domain
PLACE1009067//Src homology domain 3
PLACE1010081//Eukaryotic protein kinase domain
PLACE1010251//EGF-like domain
PLACE1010713//Alcohol/other dehydrogenases, short chain type
PLACE1010784//7 transmembrane receptor (rhodopsin family)
PLACE1010968//Fibronectin type III domain
PLACE1011181//ATPases associated with various cellular activities (AAA)
PLACE1011364//Eukaryotic protein kinase domain
PLACE1011407//Zinc finger, C2H2 type
PLACE1011708//CUB domain
PLACE1011824//Eukaryotic protein kinase domain
PLACE1011978//Zinc finger, C2H2 type
PLACE3000181//Cadherin
PLACE3000213//Sushi domain
PLACB4000354//BGF-like domain//Sushi domain
SKNMC1000082//Mitochondrial carrier proteins
THYRO1000196//Cadherin
THYRO1000580//Zinc finger, C2H2 type
THYRO1000678//Connexin
THYRO1000795//Mitochondrial carrier proteins
THYRO1000956//7 transmembrane receptor (rhodopsin family)
THYRO1001113//C2 domain
THYRO1001266//Sodium:solute symporter family
THYRO1001457//Phorbol esters / diacylglycerol binding domain//Bukaryotic protein kinase domain
THYRO1001478//EF hand
THYRO1001593//Eukaryotic protein kinase domain
THYRO1001700//Eukaryotic protein kinase domain
THYRO1001770//Eukaryotic protein kinase domain
Y79AA1000030//WW/rsp5/WWP domain containing proteins
Y79AA1000426//Transforming growth factor beta like domain
Y79AA1000777//WD domain, G-beta repeats
Y79AA1000876//Thioredoxins
Y79AA1000967//Eukaryotic protein kinase domain
Y79AA1001090//Ank repeat
Y79AA1001264//DnaJ, prokaryotic heat shock protein
Y79AA1001328//EGF-like domain

Y79AA1001427//FAD/NAD-binding domain in oxidoreductases
Y79AA1001523//Bromodomain//Zinc finger, C3HC4 type (RING finger)
Y79AA1001530//Tubulin
Y79AA1001727//IG superfamily
Y79AA1001787//E1-E2 ATPases
Y79AA1001799//Mitochondrial carrier proteins
Y79AA1002022//IG superfamily
Y79AA1002381//Eukaryotic protein kinase domain

EXAMPLE 17

Functional categories based on the full-length nucleotide sequences

[0243] Prediction of functions of proteins encoded by the clones and the categorization thereof were performed based on the results of homology search (see homology search result 10) of the databases, GenBank, Swiss-Prot and UniGene for the full-length nucleotide sequences of 826 clones as well as based on the results of domain search (see Example 16) of the deduced amino acid sequences encoded by the full-length nucleotide sequences. (HEMBA1005337, NT2RM1000407, NT2RM2001767, and NT2RP3003939 were excluded because of the absence of full-length sequence.)

[0244] There are 611 clones that presumably encode proteins belonging to any of categories of secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins and disease-associated proteins.

[0245] The clones presumably encoding proteins categorized into secretory and/or membrane proteins are those which matched the full-length sequences of Swiss-Prot database with keywords "growth factor", "cytokine", "hormone", "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel", "cell adhesion", "collagen" or "connective tissue"; those which matched the data, suggesting that the proteins are secretory and/or membrane proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those predicted to have an N-terminal signal sequence or a transmembrane region as a result of domain search for the amino acid sequences deduced from the full-length nucleotide sequences.

[0246] The clones presumably encoding proteins categorized into glycoprotein-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "glycoprotein"; those which matched the data, suggesting that the proteins are glycoprotein; or those which matched the full-length sequences of GenBank or UniGene database.

[0247] The clones presumably encoding proteins categorized into signal transduction-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "serine/threonine-protein kinase", "tyrosine-protein kinase" or "SH3 domain"; those which matched the data, suggesting that the proteins are signal transduction-associated proteins (for example, "ADP-ribosylation factor"); or those which matched the the full-length sequences of GenBank or UniGene database with similar description.

[0248] The clones presumably encoding proteins categorized into transcription-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "transcription regulation", "zinc finger" or "homeobox"; those which matched the data, suggesting that the proteins are transcription-associated proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0249] The clones presumably encoding proteins categorized into disease-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "disease mutation" or "syndrome"; those which matched the data, suggesting that the proteins are disease-associated proteins; or those which matched the full-length sequences of Swiss-Prot database and GenBank or UniGene database where the matched sequences are those of genes or proteins which had been deposited in the database of Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is a database of human genes and diseases.

[0250] The following 437 clones were categorized into secretory and/or membrane proteins.

BNGH41000020,	BNGH41000087,	BNGH41000091,	HEMBA1000121,	HEMBA1000128,	HEMBA1000349,
HEMBA1000477,	HEMBA1000590,	HEMBA1000713,	HEMBA1000732,	HEMBA1000745,	HEMBA1000835,
HEMBA1000940,	HEMBA1000962,	HEM8A1001221,	HEMBA1001228,	HEMBA1001621,	HEMBA1002131,
HEMBA1002163,	HEMBA1002167,	HEMBA1002178,	HEMBA1002195,	HEMBA1002227,	HEMBA1002420,
HEMBA1002421,	HEMBA1002767,	HEMBA1003047,	HEMBA1003101,	HEMBA1003230,	HEMBA1003392,
HEMBA1003530,	HEMBA1003602,	HEMBA1003732,	HEMBA1003945,	HEMBA1004110,	HEMBA1004250,
HEMBA1004391,	HEMBA1004444,	HEMBA1004454,	HEMBA1004505,	HEMBA1004797,	HEMBA1004982,
HEMBA1005070,	HEMBA1005449,	HEMBA1005522,	HEMBA1005545,	HEMBA1005698,	HEMBA1005945,

HEMBA1006171, HEMBA1006299, HEMBA1006311, HEMBA1006335, HEMBA1006357, HEMBA1006430, HEMBA1006482, HEMBA1006707, HEMBA1006724, HEMBA1006749, HEMBA1006902, HEMBA1006960, HEMBA1007241, HEMBB1000407, HEMBB1000447, HEMBB1000567, HEMBB1000679, HEMBB1000881, HEMBB1001026, HEMBB1001048, HEMBB1001407, HEMBB1001573, HEMBB1001573, HEMBB1001847, HEMBB1001978, HEMBB1002041, HEMBB1002162, HEMBB1002245, HEMBB1002427, HEMBB1002693, MAMMA1000102, MAMMA1000106, MAMMA1000118, MAMMA1000141, MAMMA1000204, MAMMA1000226, MAMMA1000457, MAMMA1000473, MAMMA1000496, MAMMA1000591, MAMMA1000681, MAMMA1000810, MAMMA1000986, MAMMA1000994, MAMMA1001043, MAMMA1001141, MAMMA1001237, MAMMA1001344, MAMMA1001418, MAMMA1001893, MAMMA1001957, MAMMA1001978, MAMMA1002070, MAMMA1002091, MAMMA1002095, MAMMA1002165, MAMMA1002234, MAMMA1002586, MAMMA1002633, MAMMA1003126, NT2RM1000462, NT2RM1000542, NT2RM1000580, NT2RM1000855, NT2RM1000858, NT2RM1000899, NT2RM2000241, NT2RM2000410, NT2RM2000423, NT2RM2000565, NT2RM2001626, NT2RM2001792, NT2RM2001939, NT2RM2001941, NT2RM4000198, NT2RM4000284, NT2RM4000417, NT2RM4000444, NT2RM4000587, NT2RM4000593, NT2RM4000648, NT2RM4000761, NT2RM4000997, NT2RM4001325, NT2RM4001735, NT2RM4001768, NT2RM4001843, NT2RM4002352, NT2RP1000050, NT2RP1000181, NT2RP1000261, NT2RP1000300, NT2RP1000325, NT2RP1000448, NT2RP1000551, NT2RP1000613, NT2RP1000981, NT2RP1001004, NT2RP1001563, NT2RP2000479, NT2RP2000533, NT2RP2000616, NT2RP2000649, NT2RP2000663, NT2RP2000694, NT2RP2000818, NT2RP2000903, NT2RP2001200, NT2RP2001276, NT2RP2001480, NT2RP2001495, NT2RP2001514, NT2RP2001755, NT2RP2001915, NT2RP2001956, NT2RP2002063, NT2RP2002188, NT2RP2002232, NT2RP2002527, NT2RP2002533, NT2RP2002721, NT2RP2002824, NT2RP2002942, NT2RP2002976, NT2RP2003042, NT2RP2003210, NT2RP2003383, NT2RP2003390, NT2RP2003469, NT2RP2003593, NT2RP2003655, NT2RP2003664, NT2RP2003950, NT2RP2004179, NT2RP2004205, NT2RP2004495, NT2RP2004524, NT2RP2004556, NT2RP2004606, NT2RP2004648, NT2RP2004794, NT2RP2005027, NT2RP2005163, NT2RP2005181, NT2RP2005378, NT2RP2005463, NT2RP2005541, NT2RP2005597, NT2RP2005666, NT2RP2005883, NT2RP2005994, NT2RP2006004, NT2RP2006042, NT2RP2006269, NT2RP2006512, NT2RP2006580, NT2RP3000169, NT2RP3000171, NT2RP3000304, NT2RP3000436, NT2RP3000460, NT2RP3000616, NT2RP3000676, NT2RP3000721, NT2RP3000818, NT2RP3000907, NT2RP3000921, NT2RP3001012, NT2RP3001159, NT2RP3001195, NT2RP3001240, NT2RP3001271, NT2RP3001322, NT2RP3001388, NT2RP3001560, NT2RP3001592, NT2RP3001650, NT2RP3001738, NT2RP3001858, NT2RP3002015, NT2RP3002160, NT2RP3002311, NT2RP3002342, NT2RP3002411, NT2RP3002737, NT2RP3002790, NT2RP3002836, NT2RP3002900, NT2RP3002958, NT2RP3003000, NT2RP3003076, NT2RP3003354, NT2RP3003532, NT2RP3003535, NT2RP3003614, NT2RP3004025, NT2RP3004075, NT2RP3004083, NT2RP3004130, NT2RP3004133, NT2RP3004309, NT2RP3004345, NT2RP3004406, NT2RP3004481, NT2RP3004552, NT2RP3004625, NT2RP3004647, NT2RP4001001, NT2RP4001009, NT2RP4001467, NT2RP4001879, NT2RP4002187, NT2RP4002451, NT2RP4002750, OVARC1000003, OVARC1000105, OVARC1000298, OVARC1000307, OVARC1000313, OVARC1000410, OVARC1000439, OVARC1000553, OVARC1000811, OVARC1000873, OVARC1000956, OVARC1001030, OVARC1001163, OVARC1001336, OVARC1001570, OVARC1001607, OVARC1001725, OVARC1001991, PLACE1000033, PLACE1000231, PLACE1000560, PLACE1000740, PLACE1000912, PLACE1000914, PLACE1000927, PLACE1001016, PLACE1001123, PLACE1001183, PLACE1001231, PLACE1001340, PLACE1001401, PLACE1001407, PLACE1001464, PLACE1001516, PLACE1001536, PLACE1001564, PLACE1001655, PLACE1001795, PLACE1001836, PLACE1001918, PLACE1001949, PLACE1002080, PLACE1002095, PLACE1002355, PLACE1002374, PLACE1002518, PLACE1002547, PLACE1002726, PLACE1002905, PLACE1002911, PLACE1002967, PLACE1003407, PLACE1003573, PLACE1003737, PLACE1003772, PLACE1003839, PLACE1003845, PLACE1003852, PLACE1004279, PLACE1004282, PLACE1004441, PLACE1004450, PLACE1004482, PLACE1004520, PLACE1004630, PLACE1004637, PLACE1004648, PLACE1004816, PLACE1005003, PLACE1005005, PLACE1005031, PLACE1005383, PLACE1005410, PLACE1005426, PLACE1005544, PLACE1005569, PLACE1005660, PLACE1005725, PLACE1005745, PLACE1005878, PLACE1005927, PLACE1006071, PLACE1006093, PLACE1006208, PLACE1006277, PLACE1006290, PLACE1006443, PLACE1006716, PLACE1006809, PLACE1006959, PLACE1007081, PLACE1007096, PLACE1007296, PLACE1007626, PLACE1007845, PLACE1007881, PLACE1008359, PLACE1008469, PLACE1008716, PLACE1008744, PLACE1008985, PLACE1009067, PLACE1009196, PLACE1009279, PLACE1009527, PLACE1009546, PLACE1009600, PLACE1009982, PLACE1010011, PLACE1010078, PLACE1010251, PLACE1010445, PLACE1010713, PLACE1010784, PLACE1010827, PLACE1010968, PLACE1011116, PLACE1011181, PLACE1011236, PLACE1011516, PLACE1011708, PLACE3000181, PLACE3000213, PLACE4000354, SKNMC1000004, SKNMC1000014, SKNMC1000082, THYRO1000036,

THYRO1000099, THYRO1000196, THYRO1000400, THYRO1000584, THYRO1000678, THYRO1000776, THYRO1000795, THYRO1000956, THYRO1001102, THYRO1001113,
THYRO1001205, THYRO1001237, THYRO1001242, THYRO1001266, THYRO1001327, THYRO1001456, THYRO1001478, THYRO1001523, THYRO1001529, THYRO1001641, THYRO1001702, THYRO1001725, Y79AA1000207, Y79AA1000226, Y79AA1000270, Y79AA1000426, Y79AA1000521, Y79AA1000876, Y79AA1000888, Y79AA1000959, Y79AA1001013, Y79AA1001212, Y79AA1001264, Y79AA1001328, Y79AA1001426, Y79AA1001427, Y79AA1001430, Y79AA1001727, Y79AA1001787, Y79AA1001795, Y79AA1001799, Y79AA1001803, Y79AA1002022, Y79AA1002058, Y79AA1002129, Y79AA1002213, Y79AA1002373,

[0251] The following 146 clones were categorized into glycoprotein-associated proteins.

BNGH41000087, BNGH41000091, HEMBA1000349, HEMBA1000590, HEMBA1000745, HEMBA1000835, HEMBA1001221, HEMBA1001228, HEMBA1001621, HEMBA1002131, HEMBA1002178, HEMBA1002421, HEMBA1002767, HEMBA1003230, HEMBA1003392, HEMBA1004250, HEMBA1004391, HEMBA1004444, HEMBA1004505, HEMBA1005449, HEMBA1005522, HEMBA1005545, HEMBA1006707, HEMBA1006749, HEMBA1006902, HEMBB1000679, HEMBB1000881, HEMBB1001048, HEMBB1002120, HEMBB1002245, HEMBB1002427, MAMMA1000102, MAMMA1000591, MAMMA1000681, MAMMA1001043, MAMMA1001237, MAMMA1002070, MAMMA1002586, MAMMA1003126, NT2RM1000462, NT2RM1000580, NT2RM2001792, NT2RM2001818, NT2RM2001939, NT2RM2001941, NT2RM4000198, NT2RM4000284, NT2RM4000417, NT2RM4000648, NT2RM4000997, NT2RM4001325, NT2RM4002352, NT2RP1000613, NT2RP1000981, NT2RP1001004, NT2RP2000616, NT2RP2000694, NT2RP2000903, NT2RP2001480, NT2RP2001755, NT2RP2002533, NT2RP2003042, NT2RP2003210, NT2RP2004205, NT2RP2004606, NT2RP2005027, NT2RP2005181, NT2RP2005541, NT2RP2005597, NT2RP2005883, NT2RP2006004, NT2RP2006042, NT2RP2006269, NT2RP3000304, NT2RP3000616, NT2RP3000921, NT2RP3001650, NT2RP3002160, NT2RP3002737, NT2RP3002958, NT2RP3003000, NT2RP3003532, NT2RP3004130, NT2RP3004133, NT2RP3004481, NT2RP3004552, NT2RP3004640, NT2RP4000108, NT2RP4001467, NT2RP4002750, OVARC1000003, OVARC1000553, OVARC1000811, OVARC1000873, OVARC1001336, OVARC1001607, OVARC1001991, PLACE1000033, PLACE1000740, PLACE1001016,
PLACE1001123, PLACE1001231, PLACE1001464, PLACE1001655, PLACE1001836, PLACE1002355, PLACE1002374, PLACE1002905, PLACE1002911, PLACE1003573, PLACE1003737, PLACE1003772, PLACE1003839, PLACE1004282, PLACE1004441, PLACE1004450, PLACE1004520, PLACE1004648, PLACE1005003, PLACE1005426, PLACE1006071, PLACE1006073, PLACE1006290, PLACE1007081, PLACE1007845, PLACE1008716, PLACE1008744, PLACE1008985, PLACE1010251, PLACE1010784, PLACE1010968, PLACE1011116, PLACE3000181, PLACE3000213, PLACE4000354, THYRO1000036, THYRO1000196, THYRO1000584, THYRO1000956, THYRO1001266, Y79AA1000270, Y79AA1000426, Y79AA1001727, Y79AA1001795, Y79AA1002022, Y79AA1002213,

[0252] The following 55 clones were categorized into signal transduction-associated proteins.

HEMBA1000006, HEMBA1002195, HEMBA1002227, HEMBA1002551, HEMBA1005084, HEMBA1005929, HEMBA1006658, HEMBA1006916, MAMMA1000881, MAMMA1001150, MAMMA1001310, MAMMA1002142, NT2RM2001902, NT2RP1001020, NT2RP1001031, NT2RP2001469, NT2RP2001529, NT2RP2001769, NT2RP2003179, NT2RP2003545, NT2RP2004670, NT2RP3000011, NT2RP3000022, NT2RP3000172, NT2RP3000201, NT2RP3000820, NT2RP3003527, NT2RP3003849, NT2RP3003874, NT2RP3004067, NT2RP4000634, NT2RP4000962, OVARC1000255, OVARC1000529, OVARC1000916, OVARC1001338, OVARC1001569, PLACE1002329, PLACE1003135, PLACE1003598, PLACE1005519, PLACE1006208, PLACE1008282, PLACE1008297, PLACE1010081, PLACE1011364, PLACE1011824, THYRO1001457, THYRO1001593, THYRO1001700, THYRO1001770, Y79AA1000777, Y79AA1000967, Y79AA1002376, Y79AA1002381,

[0253] The following 80 clones were categorized into transcription -associated proteins.

HEMBA1000462, HEMBA1000671, HEMBA1001297, HEMBA1001390, HEMBA1001886, HEMBA1002048, HEMBA1003120, HEMBA1003497, HEMBA1004785, HEMBA1005230, HEMBA1005246, HEMBA1006276, HEMBA1006572, HEMBA1007226, HEMBB1000106, HEMBB1000905, HEMBB1001959, HEMBB1002051, HEMBB1002661, MAMMA1001094, MAMMA1001532, MAMMA1001615, NT2RM1000789, NT2RM2000632, NT2RM2000773, NT2RM4000326, NT2RP1000271, NT2RP1000468, NT2RP2000092, NT2RP2000610, NT2RP2000712, NT2RP2000739, NT2RP2001538, NT2RP2001662, NT2RP2001817, NT2RP2001948, NT2RP2002564, NT2RP2002974, NT2RP2003138, NT2RP2003302, NT2RP2003940, NT2RP2004108, NT2RP2004847, NT2RP2005247, NT2RP2005391, NT2RP2005535, NT2RP2005774, NT2RP2005941, NT2RP2006092, NT2RP3000148, NT2RP3000232, NT2RP3000378, NT2RP3000652, NT2RP3001976, NT2RP3004090, NT2RP3004119, NT2RP3004294, OVARC1001049, OVARC1001086, OVARC1001132, OVARC1001807, PLACE1000258, PLACE1000442, PLACE1000907, PLACE1003529, PLACE1004166,

PLACE1004168, PLACE1004887, PLACE1005250, PLACE1005682, PLACE1006079, PLACE1008549, PLACE1011407, PLACE1011978, THYRO1000580, Y79AA1000030, Y79AA1001090, Y79AA1001523, Y79AA1002334, Y79AA1002378,

[0254] The following 85 clones were categorized into disease-associated proteins.

BNGH41000020, HEMBA1000349, HEMBA1000590, HEMBA1000671, HEMBA1000835, HEMBA1001184, HEMBA1001228, HEMBA1001886, HEMBA1003120, HEMBA1004250, HEMBA1005246, HEMBA1005267, HEMBA1006707, HEMBA1006749, HEMBA1006902, HEMBA1006916, HEMBA1007013, HEMBB1002120, MAMMA1000204, MAMMA1002080, NT2RM2000632, NT2RM2001126, NT2RM2001558, NT2RP1000271, NT2RP1000465, NT2RP1000579, NT2RP2000447, NT2RP2000514, NT2RP2000739, NT2RP2001223, NT2RP2001529, NT2RP2001562, NT2RP2002674, NT2RP2003369, NT2RP2004108, NT2RP2004205, NT2RP2005535, NT2RP2005941, NT2RP2006004, NT2RP3000059, NT2RP3000125, NT2RP3000201, NT2RP3000232, NT2RP3000616, NT2RP3000677, NT2RP3000838, NT2RP3000921, NT2RP3001542, NT2RP3002286, NT2RP3002721, NT2RP3002737, NT2RP3002738, NT2RP3004481, OVARC1000208, OVARC1000275, OVARC1000331, OVARC1000410, OVARC1001086, OVARC1001132, OVARC1001607, OVARC1001725, OVARC1001952, PLACE1000258, PLACE1000442, PLACE1000907, PLACE1001100, PLACE1001500, PLACE1002905, PLACE1002967, PLACE1003407, PLACE1003428, PLACE1005005, PLACE1005239, PLACE1005815, PLACE1007028, PLACE1008716, PLACE1011407, PLACE1011978, PLACE2000118, THYRO1000580, THYRO1000866, THYRO1001071, THYRO1001478, Y79AA1001062, Y79AA1001530,

[0255] Out of them, the following 67 clones are those which matched the data of Swiss-Prot database and GenBank or UniGene database, genes or proteins which had been deposited in the database of Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nim.nih.gov/Omim/), which is a database of human genes and diseases. (The corresponding OMIM numbers are indicated after the clone names.)

HEMBA1000349(*600046), HEMBA1000590(*603897), HEMBA1000671(*602277), HEMBA1001886(*603899), HEMBA1003120(*602277), HEMBA1004250(*600976), HEMBA1005246(*602291), HEMBA1005267(*106410), HEMBA1006707(*603897), HEMBA1006749(*603897), HEMBA1006902(*603897), HEMBA1006916(*601524), HEMBA1007013(*603730), HEMBB1002120(*603367), MAMMA1002080(*602672), NT2RM2001126(*603785), NT2RM2001558(*604689), NT2RP1000271(*603899), NT2RP1000465(*602231), NT2RP2000447(*602580), NT2RP2000514(*602431), NT2RP2000739(*194558), NT2RP2001223(*603558), NT2RP2001529(*603289), NT2RP2001562(*603371), NT2RP2002674(*132811), NT2RP2003369(*179555), NT2RP2004108(*601260), NT2RP2004205(*601610), NT2RP2005535(*603899), NT2RP2006004(*600245), NT2RP3000059(*106410), NT2RP3000125(*180202), NT2RP3000201(*604666), NT2RP3000232(*602277), NT2RP3000616(*600245), NT2RP3000677(*142765), NT2RP3000838(*190370), NT2RP3001542(*191161), NT2RP3002286(*604331), NT2RP3002721(*118950), NT2RP3002738(*602265), NT2RP3004481(*601610), OVARC1000208(*603603), OVARC1000275(*125647), OVARC1000331(*139265), OVARC1000410(*603874), OVARC1001086(*603862), OVARC1001725(*603046), OVARC1001952(*190370), PLACE1000258(*603971), PLACE1000442(*601260), PLACE1000907(*194558), PLACE1001500(*603781), PLACE1002905(*125950), PLACE1003428(*603570), PLACE1005005(*603124), PLACE1005239(*603365), PLACE1007028(*602131), PLACE1011407(*602277), PLACE1011978(*603971), PLACE2000118(*301000), THYRO1000580(*602277), THYRO1000866(*604045), THYRO1001071(*603533), Y79AA1001062(*191161), Y79AA1001530(*602662).

[0256] Out of 215 clones excluding the above-mentioned clones, HEMBB1000668 and NT2RM4001377 presumably belong to a group of signal transduction-associated proteins, based on the results of domain search by Pfam.

[0257] HEMBB1002302 presumably belong to a group of transcription-associated proteins, based on the results of domain search by Pfam.

[0258] In the 437 clones categorized into secretory and/or transmembrane proteins on the basis of their full-length sequences, 410 clones were also predicted to encode proteins having functions of secretory and/or membrane proteins on the basis of their partial nucleotide sequences (5' sequences). In the 146 clones categorized into glycoprotein-associated proteins on the basis of their full-length sequences, 124 clones were also predicted to encode proteins having functions of glycoprotein-associated proteins on the basis of their partial nucleotide sequences. In the 57 clones categorized into signal transduction-associated proteins on the basis of their full-length sequences, 46 clones were also predicted to encode proteins having functions of signal transduction-associated proteins on the basis of their partial nucleotide sequences. In the 81 clones categorized into transcription-associated proteins on the basis of their full-length sequences, 57 clones were also predicted to encode proteins having functions of transcription-associated proteins on the basis of their partial nucleotide sequences. In the 85 clones categorized into disease-associated proteins on the basis of their full-length sequences, 6 clones were also predicted to encode proteins having functions of disease-associated proteins on the basis of their partial nucleotide sequences. The number of clones which were predicted to encode disease-associated proteins based on the full-length nucleotide sequences is much greater than that predicted based on the partial sequences. The reason is that the full-length sequences were categorized by using the data found

in the OMIM database into the category of disease-associated proteins.

[0259] When the predicted functions based on the partial sequences were different from those based on the full-length sequences, several reasons were presumed; the ORF is too short in the partial sequence as compared with that of the full-length sequence; alternatively, P value for the partial sequence was greater than that for the full-length, that is, as compared with the probability of occurrence of the predicted function found in the full-length sequence, the probability was lower in the partial sequence. A protein does not always belong solely to a single category of the above-described functional categories, and therefore, additional functions can be found for the cDNA clones by further analyses.

[0260] It is unclear, by the analyses for the full-length sequences so far, whether or not the remaining 212 clones encode proteins belonging to any of the categories of secretory and/or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins or disease-associated proteins. Nonetheless, the functions which were predicted based on the partial sequences can be verified by further analyses.

[0261] Among the 212 clones, there are 38 clones that presumably belong to the category of enzymes and/or metabolism-associated proteins; cell division- and/or cell proliferation-associated proteins, cytoskeleton-associated proteins, nuclear proteins, DNA-and/or RNA-binding proteins, ASP- and/or GTP-binding proteins, protein synthesis- and/or protein transport-associated proteins, or cellular defense-associated proteins. The clones containing results of homology search of Swiss-Prot database were categorized by considering the keywords and mentioned items in the matching data. The clones containing results of homology search of GenBank or UniGene database were categorized by considering the definitions and mentioned items in the matching data.

When the matching data contained keywords such as "metabolism", "oxidoreductase" and "E.C. No. (Enzyme commission number)", the clones were herein defined as clones presumably belonging to the category of enzymes and/or metabolism-associated proteins. When the matching data contained keywords such as "cell division", "cell cycle", "mitosis", "chromosomal protein", "cell growth" and "apoptosis", the clones were herein defined as clones presumably belonging to the category of cell division- or cell proliferation-associated proteins. When the matching data contained keywords such as "structural protein", "cytoskeleton", "actin-binding" and "microtubules", the clones were herein defined as clones presumably belonging to the category of cytoskeleton-associated proteins. When the matching data contained keywords such as "nuclear protein", the clones were herein defined as clones presumably belonging to the category of nuclear proteins. When the matching data contained keywords such as "DNA-binding" and "RNA-binding", the clones were herein defined as clones presumably belonging to the category of DNA- or RNA-binding proteins. When the matching data contained keywords such as "ATP-binding" and "GTP-binding", the clones were herein defined as clones presumably belonging to the category of ATP- and/or GTP-binding proteins. When the matching data contained keywords such as "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", "protein transport" and "signal recognition particle", the clones were herein defined as clones presumably belonging to the category of protein synthesis- and/or protein transport-associated proteins. When the matching data contained keywords such as "heat shock", "DNA repair" and "DNA damage", the clones were herein defined as clones presumably belonging to the category of cellular defense-associated proteins.

[0262] The following 10 clones presumably belong to enzymes and/or metabolism-associated proteins.
HEMBA1003315, HEMBB1002465, MAMMA1000614, NT2RP2000178, NT2RP2001388, NT2RP2001903, NT2RP2002304, NT2RP2005878, NT2RP3001685, PLACE1006219

[0263] The following 4 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins.
MAMMA1000403, NT2RM2000497, NT2RP2000394, Y79AA1002121

[0264] The following 6 clones presumably belong to cytoskeleton-associated proteins.
MAMMA1001609, NT2RM2000589, NT2RP3000063, PLACE1004078, PLACE 1004492, PLACE 1008657

[0265] The following 7 clones presumably belong to nuclear proteins.
HEMBA1001878, HEMBA1002992, MAMMA1000614, NT2RM4000965, NT2RM2001738, NT2RP2001388, Y79AA1002121

[0266] The following 5 clones presumably belong to DNA- and/or RNA-binding proteins.
HEMBA1003072, HEMBA1006770, HEMBA1007332, NT2RM2000497, Y79AA1002121

[0267] The following 7 clones presumably belong to ATP- and/or GTP-binding proteins.
HEMBA1002316, MAMMA1001609, NT2RM2000306, NT2RM2000497, NT2RP2000178, NT2RP3003729, PLACE1004305

[0268] The following 7 clones presumably belong to protein synthesis- and/or protein transport-associated proteins.
NT2RM4000965, NT2RP2005069, NT2RP3000481, NT2RP3000789, NT2RP4001877, OVARC1001833, OVARC1002058.

[0269] The following clone presumably belongs to cellular defense-associated proteins.
PLACE 1005539

[0270] Although it is unclear whether or not 26 out of 174 clones other than the above-mentioned clones belong to

any of the above-described categories, these clones are predicted to have some functions, based on the homology search using their full-length sequences. The clone names and the gene definitions found in the result of homology search are shown below, separated by a double-slash,//

HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.
HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.
HEMBA1003399//MVP1 PROTEIN,
HEMBA1005489//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA, complete cds.
HEMBB1000542//Mus musculus bromodamain-containing protein BP75 mRNA, complete cds.
MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds.
MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.
NT2RM2000514//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.
NT2RM2000622//Mus musculus F-box protein FBL10 mRNA, partial cds.
NT2RM4000100//Homo Sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.
NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.
NT2RP3001170//Mus musculus activity-dependent neuroprotective protein (Adnp) mRNA, complete cds.
NT2RP3002571//Bos taurus mRNA for lyncein.
NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.
OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds.
PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.
PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.
PLACE1005736//Human mRNA for BAS-GRIP protein.
PLACE1007702//Mus musculus TRA1 mRNA, complete cds.
PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.
THYRO1000061//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.
THYRO1000964//Drosophila melanogaster Felle associated protein Pellino (Pli) mRNA, complete cds.
Y79AA1000776//Mus musculus mRNA for GSG1, complete cds.
Y79AA1001056//Homo sapiens MAID protein mRNA, complete cds.
Y79AA1001272//Homo sapiens retinoic acid repressible protein (RARG-1) mRNA, complete cds.
Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.

[0271] So far, useful information for presuming the functions are unavailable for the remaining 148 clones, of which names are listed below.

HEMBA1000275, HEMBA1000300, HEMBA1000443, HEMBA1000875, HEMBA1000907, HEMBA1001272, HEMBA1001296, HEMBA1001563, HEMBA1002164, HEMEA1002239, HEMBA1002985, HEMBA1003294, HEMBA1003487, HEMBA1004007, HEMBA1004067, HEMBA1004085, HEMBA1004952, HEMBA1004971, HEMBA1005145, HEMBA1005430, HEMBA1005913, HEMBA1006016, HEMBA1006517, HEMBA1006544, HEMBA1006912, HEMBA1007057, HEMBA1007063, HEMBA1007291, HEMBB1000276, HEMBB1000309, HEMBB1000642, HEMBB1001200, HEMBB1001547, HEMBB1002039, HEMBB1002228, HEMBB1002663, MAMMA1000046, MAMMA1000449, MAMMA1000528, MAMMA1000652, MAMMA1000706, MAMMA1000814, MAMMA1001066, MAMMA1001284, MAMMA1001623, MAMMA1001634, MAMMA1001901, MAMMA1002087, MAMMA1002205, MAMMA1002224, NT2RM2000582, NT2RM2001643, NT2RM4000115, NT2RM4000295, NT2RM4001321, NT2RP1000002, NT2RP1000239, NT2RP1000679, NT2RP1000740, NT2RP1000903, NT2RP2000240, NT2RP2001878, NT2RP2001921, NT2RP2002015, NT2RP2002409, NT2RP2002510, NT2RP2003599, NT2RP2003931, NT2RP2004069, NT2RP2004141, NT2RP2004447, NT2RP2004837, NT2RP2005514, NT2RP2005632, NT2RP2005887, NT2RP2006099, NT2RP2006134, NT2RP3000427, NT2RP3000444, NT2RP3000645, NT2RP3000871, NT2RP3001044, NT2RP3001061, NT2RP3001754, NT2RP3002281, NT2RP3002324, NT2RP3002353, NT2RP3002409, NT2RP3002448, NT2RP3002664, NT2RP3002887, NT2RP3002983, NT2RP3003448, NT2RP3003469, NT2RP3003473, NT2RP3003559, NT2RP3003963, NT2RP3004000, NT2RP3004202, NT2RP3004321, NT2RP3004355, NT2RP3004374, NT2RP4002715, OVARC1000090, OVARC1000137, OVARC1000467, OVARC1000775, OVARC1000853, OVARC1000995, OVARC1001222, OVARC1001260, OVARC1001727, OVARC1002178, PLACE1000986, PLACE1001114, PLACE1001229, PLACE1001788, PLACE1003438, PLACE1003460, PLACE1003644, PLACE1004028, PLACE1004199, PLACE1004519, PLACE1005601. PLACE1005669, PLACE1005768, PLACE1006515, PLACE1006786, PLACE1007040, PLACE1007077, PLACE1007591, PLACE1007971, PLACE1008984, PLACE1009735, PLACE2000219, PLACE4000455, THYRO1000846, THYRO1000999, THYRO1001063, THYRO1001128, THYRO1001471, THYRO1001495,

THYRO1001608, THYRO1001803, Y79AA1000127, Y79AA1000750, Y79AA1001592, Y79AA1001863,

EXAMPLE 18

Expression frequency analysis using PCR

[0272] Many genes acting at the downstream of TNF-. and IL-1. among inflammation-associated cytokines have been previously identified. The respective stimulations are transduced through independent pathways of signaling cascade. There exists another signaling cascade for both stimulations, wherein NF-.B is a common transducing molecule shared by the two stimulations (J. Leukoc. Biol., 1994, 56(5): 542-547). It has also been revealed that many inflammation-associated genes, including IL-2, IL-6 and G-CSF, are varied in their expression levels in response to the signal through the common pathway (Trends Genet. 1999, 15(6): 229-235). A survey was performed by using ATAC-PCR method (adaptor-competitive PCR method: Nucleic Acids Res. 1997, Nov 15; 25(22): 4694-6) for genes of which expression levels were varied depending on stimulation of inflammatory cytokines, TNF-. and IL-1.. It is possible that genes of which expression is varied in response to this stimulation also participate in inflammation.

[0273] Jurkat cells (Dainippon Pharmaceutical Co., Ltd.: catalog No. 06-152) were cultured in a PRMI1640 medium (Nikken Biological and Medical Institute: catalog No. 14-501F) containing 10% fetal calf serum until the cell count reached 10^7 cells. The cells were transferred into a fresh medium containing 10 ng/ml TNF-. (recombinant Tumor Necrosis Factor; Wako pure chemical Industries Inc.: catalog No. 201-13461) or IL-1. (recombinant Interleukin-1.; PeprotechEC: catalog No. 200-01B) and, further, cultured at 37. under an atmosphere of 5% CO_2. The cells cultured in the presence of TNF-. were harvested 1, 3 and 7 hours after addition of TNF-.. The cells cultured in the presence of IL-1. were harvested 1 and 7 hours after addition of IL-1.. Total RNA was extracted from each of the cells by AGPC method (Acid-Guanidinium-Phenol-Chloroform method: Ana Biochem. 1987, Apr; 162(1):156-9). Total RNA was also extracted form the cells in the absence of any stimulation of TNF-. and IL-1

[0274] ATAC-PCR analysis is performed basically according to the same procedure as described in "DNA Microarray and Advanced PCR Methods" (Cell Engineering, p. 104-112, (additional volume, Genome Science Series 1), Muramatsu & Naba (eds.), Shujunnsya). Adaptor ligation reaction was performed for an internal standard sample (which was used for preparing a calibration curve for the assessment of the test samples) and test samples in the following independent two reaction systems. Combinations of each type of the 6 adaptors (AD-1, AD-2, AD-3, AD-4, AD-5, and AD-6: see the sequences shown below) with each sample are as follows:

Reaction system A

AD1: internal standard sample (x10 concentration)
AD2: sample before stimulation
AD3: internal standard sample (x3 concentration)
AD4: sample with IL-1 stimulation for 1 hour
AD5: sample with IL-1 stimulation for 7 hours
AD6: internal standard sample (x1 concentration)

Reaction system B

AD1: internal standard sample (x1 concentration)
AD2: sample with TNF stimulation for 1 hour
AD3: sample with TNF stimulation for 3 hours
AD4: internal standard sample (x3 concentration)
AD5: sample with TNF stimulation for 7 hours
AD6: internal standard sample (x10 concentration)

Adaptor sequence

AD1;

SEQ ID NO:4180//5'-GTACATATTCTCGTTAGAACGCG-3'

SEQ ID NO:4181//3'-CATGTATAACAGCAATCTTGCGCCTAG-5'

AD2;

SEQ ID NO:4182//5'-GTACATTGTCGTTAGAACGCGACT-3'

SEQ ID NO:4183//3'-CATGTATAACAGCAATCTTGCGCTGACTAG-5'

AD3;

SEQ ID NO:4184//5'-GTACATATTGTCGTTAGAACGCGCATACT-3'

SEQ ID NO:4185//3'-CATGTATAACAGCAATCTTGCGCGTATCACTAG-5'

AD4;

SEQ ID NO:4186//5'-GTACATATTGTCGTTAGAACGCGATCCATACT-3'

SEQ ID NO:4187//3'-CATGTATAACAGCAATCTTGCGCTAGGTATGACTAG-5'

AD5;

SEQ ID NO:4188//5'-GTACATATTGTCGTTAGAACGCGTCAATCCATACT-3'

SEQ ID NO:4189//3'-CATGTATAACAGCAATCTTGCGCAGTTAGGTATGACTAG-5'

AD6;

SEQ ID NO:4190//5'-GTACATATTGTCGTTAGAACGCGTACTCAATCCATACT-3'

SEQ ID NO:4191//3'-CATGTATAACAGCAATCTTGCGCATGAGTTAGGTATGACTAG-5'

[0275] In this assay, the internal standard samples used were total RNA from cultured cells or human tissues from which the cDNA libraries originated. The cultured cells and the total RNAs from tissues are indicated below. Culture of the cells was performed according to the method as described in the supplier's instruction manual. RNA preparation was carried out by standard methods.

Human teratocarcinoma cell NT-2 (Stratagene, catalog No. 204101)
Human neuroblastoma cell SK-N-MC (Dainippon Pharmaceutical Co., Ltd., catalog No. 04-010)
Human neuroblastoma cell Y79 (Dainippon Pharmaceutical Co., Ltd., catalog No. 04-018)
Human placenta tissues total RNA (BioChin, catalog No. 064008)
Human breast tissue total RNA (Clontech, catalog No. 64037-1)

[0276] PCR primers used for amplification of specific genes, and names of the corresponding cDNA clones are shown below. The assay was not carried out for clones of which corresponding internal standard sample could not be prepared for the assay. The gene-specific primers were designed so that the PCR products derived from the cDNAs with adaptor were 70-200 bp in size. Sequence of the adaptor-specific primer (labeled with fluorescent dye (FAM)) used for the competitive PCR was GTACATATTGTCGTTAGAACGC (22 nucleotides, SEQ ID NO: 4192). PCR was performed basically at 94. for 5 minutes; and at 94. for 30 seconds, at 50. for 60 seconds, and at 72. for 60 seconds for 30 cycles. The annealing temperature was, however, changed in some PCR experiments.

[0277] Nucleotide sequence of clone-specific primer (all the primers consist of 20 nucleotides) used in this experiment

[0278] Clone names, primer sequences, and SEQ ID NOs were shown in this order, separated with a double-slash mark, //

MAMMA1000046//GTTACATCCAAGCATACAGG//SEQ ID NO:4193
MAMMA1000102//ACGGGGTCTCATTCTGACAC//SEQ ID NO:4194
MAMMA1000141//CAAGGTAACACGAGTCTATC//SEQ ID NO:4195
MAMMA1000226//ACTGAGGGGCAAAGGAGAGA//SEQ ID NO:4196
MAMMA1000403//ATTTTCCTGGAGAGCCGACT//SEQ ID NO:4197
MAMMA1000473//TGGAAAGTGTACCGGAATTG//SEQ ID NO:4198
MAMMA1000495//TCAATCTGGCGCTCTGTCAC//SEQ ID NO:4199
MAMMA1000614//AGTTCTTTACATGCTGAGGT//SEQ ID NO:4200
MAMMA1000652//TGGTGGAAGACTGGGTTTGC//SEQ ID NO:4201
MAMMA1000705//ATGGTCTTGTGGTGCCAGGT//SEQ ID NO:4202
MAMMA1000788//TGTCCAAAAGCCACACAGAG//SEQ ID NO:4203
MAMMA1000810//ATACTTCCCGCACCCCAAAA//SEQ ID NO:4204
MAMMA1000814//CAGGGTTTCTGCATGTTGGC//SEQ ID NO:4205
MAMMA1000881//ATGGAGTTTCACTCTTGTTG//SEQ ID NO:4206
MAMMA1000986//TGCTGCTTCTTTACATGGGA//SEQ ID NO:4207
MAMMA1000994//CAGGATAGAGGTTGCAGGCT//SEQ ID NO:4208
MAMMA1001066//GATGGGGTCTCACTCTGTCA//SEQ ID NO:4209
MAMMA1001094//ACGTCCAGAAACTACAGGGT//SEQ ID NO:4210
MAMMA1001141//ACTGTACTTAGGATGCTTCA//SEQ ID NO:4211
MAMMA1001237//GGGCAACCCTATGTAGATGA//SEQ ID NO:4212
MAMMA1001284//GTCTGCTCTGTTACATAGGG//SEQ ID NO:4213
MAMMA1001310//ACGCCTGTAATCCCAACCCA//SEQ ID NO:4214
MAMMA1001344//GCCAGTTTGTTCTAGGATGC//SEQ ID NO:4215
MAMMA1001532//ACATCTATAAGGCTGTTTGC//SEQ ID NO:4216
MAMMA1001609//GGGTCTCACTCTGTTACCCA//SEQ ID NO:4217
MAMMA1001615//CAAGGGACACTGAGAACTGC//SEQ ID NO:4218
MAMMA1001623//GGATTGATGCCCGATACTTA//SEQ ID NO:4219
MAMMA1001901//GATAGGGTCTCATTCTGTTA//SEQ ID NO:4220
MAMMA1001957//TAGTAGAGACGGGGTTTCAC//SEQ ID NO:4221
MAMMA1001978//CTCCCTCAGACGCTTTATTG//SEQ ID NO:4222
MAMMA1002070//GAAGAGAAACTGCGGCATCC//SEQ ID NO:4223
MAMMA1002080//ACTCTCCCTCACTACCACTG//SEQ ID NO:4224
MAMMA1002087//AGCTCGTCTCATGGGCAACT//SEQ ID NO:4225
MAMMA1002091//CTGACGTAGGTGAGGTCCAT//SEQ ID NO:4226

MAMMA1002095//CATGTTTATGGTCAGCTAGT//SEQ ID NO:4227
MAMMA1002128//TGCAGCAGATGAGCAAGCAC//SEQ ID NO:4228
MAMMA1002142//TCTCTTAAACATGCAACAGG//SEQ ID NO:4229
MAMMA1002165//CTCAAACACCCAGCGCTCAAG//SEQ ID NO:4230
MAMMA1002234//TTTGTCTTCCTCTAAACCAG//SEQ ID NO:4231
MAMMA1002586//CTCCACCGAAAAGACCCATT//SEQ ID NO:4232
MAMMA1002633//CACAGCAGCATCTCCAAGCA//SEQ ID NO:4233
MAMMA1003126//ACAGTATCAGAGGAGCAGGA//SEQ ID NO:4234
NT2RM1000462//AGAGCCGAGGACATTTGAGG//SEQ ID NO:4235
NT2RM1000542//CAAGGGCACGTTTCAGCACT//SEQ ID NO:4236
NT2RM1000789//TTCCCTTGCTCTTCTCTGGA//SEQ ID NO:4237
NT2RM1000855//AGCAAGGTCTCCAGAGTGTG//SEQ ID NO:4238
NT2RM1000858//GAACAGGAAAATGCTCTCAG//SEQ ID NO:4239
NT2RM2000241//CTGCTTGCCTGCCTTGTAGT//SEQ ID NO:4240
NT2RM2000306//TAGTCCCTTTCCTGATGGTC//SEQ ID NO:4241
NT2RM2000497//TTAGTAGAGACGGTGTTTCA//SEQ ID NO:4242
NT2RM2000514//TGTTCTCTTTCTTTCCACTG//SEQ ID NO:4243
NT2RM2000562//GGGAATAACATCTACAACCT//SEQ ID NO:4244
NT2RM2000588//CCCCAGAAACAGAGAAGGCT//SEQ ID NO:4245
NT2RM2000589//TAAGGCATGTGTCCTCTAAG//SEQ ID NO:4246
NT2RM2000622//ATCTCGGCTATGAACTGCTC//SEQ ID NO:4247
NT2RM2000773//TTCTGCCCCTCCTCAAACCT//SEQ ID NO:4248
NT2RM2001126//CCAACAGCTTCTTCATGGGT//SEQ ID NO:4249
NT2RM2001558//TCGCCCACACTGCATCCTTT//SEQ ID NO:4250
NT2RM2001626//TCGGGTGGCAGTGTGTTGAA//SEQ ID NO:4251
NT2RM2001643//GTAGTTCTCTCTGAAGAATC//SEQ ID NO:4252
NT2RM2001738//CCCAGCACTTTTATTTGTAG//SEQ ID NO:4253
NT2RM2001792//AGTGTAGTTTGGAGATGAGA//SEQ ID NO:4254
NT2RM2001902//TCCCCATCCAGCCACAGAAA//SEQ ID NO:4255
NT2RM2002109//ATTGCCTATAGAAAGTCAGC//SEQ ID NO:4256
NT2RM4000100//CCATTTATAGCGCTCAAGAT//SEQ ID NO:4257
NT2RM4000115//TAGTTTCGACTTCTGGTTCA//SEQ ID NO:4258
NT2RM4000284//ACATCCTTCAAATCAGCATC//SEQ ID NO:4259
NT2RM4000295//GGTCTCACGCTGCTCACAAA//SEQ ID NO:4260
NT2RM4000417//TGCTGTGTAGTATTCCTTAG//SEQ ID NO:4261
NT2RM4000761//CTAATACAATGCCAGTCAGG//SEQ ID NO:4262
NT2RM4001377//CTAGCTTCCTCTCCCAACTG//SEQ ID NO:4263
NT2RM4001735//TCATCACGACTGCTGTAGAG//SEQ ID NO:4264
NT2RM4001768//TTAGTAGAGCTGGGCTTTCA//SEQ ID NO:4265

NT2RM4001843//CAAGGGCACGTTTCAGCACT//SEQ ID NO:4266
NT2RP1000239//TTAGCAGTCTATCCTTTCCG//SEQ ID NO:4267
NT2RP1000465//TTGCCCAGGCTAGTCTCGAA//SEQ ID NO:4268
NT2RP1000468//TTGCCCAGGCTAGTCTCGAA//SEQ ID NO:4269
NT2RP1000679//GGCCTCAGTTCCTTGCATTT//SEQ ID NO:4270
NT2RP1000740//CGCTATATTTCATGGCTTT//SEQ ID NO:4271
NT2RP1001031//CATGTTAGCTATACACACCA//SEQ ID NO:4272
NT2RP2000092//CACACACACATGAACTCATT//SEQ ID NO:4273
NT2RP2000178//ATCTTTTGTGACAGCTCCAG//SEQ ID NO:4274
NT2RP2000240//CCATTCCACTCATACCAAGA//SEQ ID NO:4275
NT2RP2000447//CTCTTGGCATCATAGGTCTT//SEQ ID NO:4276
NT2RP2000610//GACATGAGACAAAATTACCC//SEQ ID NO:4277
NT2RP2000616//AAAATAACTCCCTGGCAGGT//SEQ ID NO:4278
NT2RP2000712//CAAGGTAGAGCTTGAGAGAG//SEQ ID NO:4279
NT2RP2000739//AGGAACAGGGAATGGAGGTG//SEQ ID NO:4280
NT2RP2000818//GGGAACAAATGAGACAAAGA//SEQ ID NO:4281
NT2RP2001200//AGCACATAGCTGCAGGAAAG//SEQ ID NO:4282
NT2RP2001276//TTGCCGTTGGTGCTGGTAGT//SEQ ID NO:4283
NT2RP2001388//TGGCACAATCTCCGGTCACT//SEQ ID NO:4284
NT2RP2001469//TAATGGGTGGTCGGAGCTGA//SEQ ID NO:4285
NT2RP2001538//CAAAAGCGTAGGCAGCAAGG//SEQ ID NO:4286
NT2RP2001562//CACCCTGCCACAAGACATTT//SEQ ID NO:4287
NT2RP2001662//AAGAGGCTGCCCAAATGGCA//SEQ ID NO:4288
NT2RP2001755//CAACCAAATAATCCAGCCAT//SEQ ID NO:4289
NT2RP2001817//CTAAAGCAACAGAGGAATAG//SEQ ID NO:4290
NT2RP2001921//TGTGGGGTTGGTCTTTGGAA//SEQ ID NO:4291
NT2RP2001948//GCATTGAGGACTTTTCCAGA//SEQ ID NO:4292
NT2RP2002015//GTAGTTCTCTCTGAAGAATC//SEQ ID NO:4293
NT2RP2003138//ATGGAAGAGGCTGAGGCAAA//SEQ ID NO:4294
NT2RP2003194//CACCTCTCATGTTTCTGCAC//SEQ ID NO:4295
NT2RP2003302//AGAGGACAGTTGGAAGATTT//SEQ ID NO:4296
NT2RP2003390//CTGTGGGTGATTTTCTGGCA//SEQ ID NO:4297
NT2RP2003593//CTGACCCCTAAGTAAATCAA//SEQ ID NO:4298
NT2RP2003664//GGGTGTGATGTTACTTCTC//SEQ ID NO:4299
NT2RP2003950//CTGAAGGAGGTACTGACACT//SEQ ID NO:4300
NT2RP2004069//CATCACCAAGGTATTAAGCC//SEQ ID NO:4301
NT2RP2004108//GATAGGTTACTGGTGAATTC//SEQ ID NO:4302
NT2RP2005069//GAAAATGAACCTGTAGCGTT//SEQ ID NO:4303
NT2RP2005378//ATTCTGGCTCCCTCTTCCTC//SEQ ID NO:4304

NT2RP2005391//CAAGGTGCATTTACATGGG//SEQ ID NO:4305
NT2RP2005535//GAATTATCGCCATGTCTCTT//SEQ ID NO:4306
NT2RP2005597//GACCAAGACCCTTCAACCTC//SEQ ID NO:4307
NT2RP2006092//TCCTACGTTGTGGTGCAGTG//SEQ ID NO:4308
NT2RP2006134//TGACTGCCAATTAGAAACCT//SEQ ID NO:4309
NT2RP2006208//AAAATTGGCTTCTGCCTAGT//SEQ ID NO:4310
NT2RP2006476//GTTCACCTTCACATCCAAAA//SEQ ID NO:4311
NT2RP3000011//TGGCACAATCTCAGCTCACT//SEQ ID NO:4312
NT2RP3000031//TTCTGGGCTGGAGTAGTGGT//SEQ ID NO:4313
NT2RP3000063//ACATAGTCACATAGACAGAG//SEQ ID NO:4314
NT2RP3000125//ACACATCCAACCCTTCACTT//SEQ ID NO:4315
NT2RP3000148//AACAAGTCCAGCCCCAGAAG//SEQ ID NO:4316
NT2RP3000169//CCAAGCACCCCATATGAAGC//SEQ ID NO:4317
NT2RP3000171//CAGAATTTGCCACGAGGAT//SEQ ID NO:4318
NT2RP3000172//GGCACAGACACCATCCTTGA//SEQ ID NO:4319
NT2RP3000201//AATGGGGTTTTGCCAGGTTG//SEQ ID NO:4320
NT2RP3000232//ACCTTCATACAACTTTTCCC//SEQ ID NO:4321
NT2RP3000304//TGGTCTGCCTCATCCTTCTC//SEQ ID NO:4322
NT2RP3000378//GAAAACGGTAGGCAGCAAGG//SEQ ID NO:4323
NT2RP3000427//ATGTAAAGTGTGGAGTACCC//SEQ ID NO:4324
NT2RP3000444//TTCTTCTCAGTCACCTCCAC//SEQ ID NO:4325
NT2RP3000616//GTGATAGTAACACAATCCTG//SEQ ID NO:4326
NT2RP3000645//TGGCCAGTGTATGAGAGGTC//SEQ ID NO:4327
NT2RP3000676//CAAGACAACAAAACAGAAGG//SEQ ID NO:4328
NT2RP3000677//TCCATTTTAGCTGTAGACAC//SEQ ID NO:4329
NT2RP3000721//GAGACTGTGATGCCTTGGTG//SEQ ID NO:4330
NT2RP3000769//AACTGATGGCTTCTGTCTCC//SEQ ID NO:4331
NT2RP3000818//GCGAGAAGCCTAGAAAACAA//SEQ ID NO:4332
NT2RP3000820//TCACATTCAAGCTCTACGTC//SEQ ID NO:4333
NT2RP3000838//CTAGCTTCCTCTCCCAACTG//SEQ ID NO:4334
NT2RP3000871//CATTGTGCTTGGAGCTTGGC//SEQ ID NO:4335
NT2RP3000907//GCGACATGAACAGGAAGCAG//SEQ ID NO:4336
NT2RP3000921//ACATGGGTAGCACTCCTTTT//SEQ ID NO:4337
NT2RP3001012//ACCCATTTCTACCTCTCTTA//SEQ ID NO:4338
NT2RP3001044//AGCAAGGCAATGAGGATACT//SEQ ID NO:4339
NT2RP3001159//AAATGTAGGCGTGGCGAAGT//SEQ ID NO:4340
NT2RP3001240//AGCAAGGTCTCCAGAGTGTG//SEQ ID NO:4341
NT2RP3001271//GTGCTTCTACCATTGAGGAT//SEQ ID NO:4342
NT2RP3001542//TGGTCCTCACTGCCTTCAAA//SEQ ID NO:4343

NT2RP3001560//CGCCTCCACAAACAAACCCT//SEQ ID NO:4344
NT2RP3001592//TAAAACGGAGGATGTTCAGT//SEQ ID NO:4345
NT2RP3001650//GCATCTTCTGGTAGTTGTCC//SEQ ID NO:4346
NT2RP3001685//GATTCTCCTTGCCTCACCCT//SEQ ID NO:4347
NT2RP3001754//AGTTAGTGGTGCCTGCTTCC//SEQ ID NO:4348
NT2RP3001976//CTCACTGGCATTTAGCTGGT//SEQ ID NO:4349
NT2RP3002015//CAACAACCTTCCTCCTACCC//SEQ ID NO:4350
NT2RP3002281//TAAACAGTCAACCAATGCTC//SEQ ID NO:4351
NT2RP3002286//AACCAAGAGATTTGGAGGAA//SEQ ID NO:4352
NT2RP3002353//GGCTGCAACTCAATTTCTCC//SEQ ID NO:4353
NT2RP3002409//GTACCCCTAGTGAAGACCTG//SEQ ID NO:4354
NT2RP3002411//TCAATAGCTACCTGTAGAGT//SEQ ID NO:4355
NT2RP3002448//TCTTCCTACGACATAACCAT//SEQ ID NO:4356
NT2RP3002571//GCCCAAAATCCAACAGTAAA//SEQ ID NO:4357
NT2RP3002721//AGTGGCTGTATTCTGTGGA//SEQ ID NO:4358
NT2RP3002737//GTGAGGTACTTGCATATCCG//SEQ ID NO:4359
NT2RP3002738//TCCCCCATGAACACCAGCTT//SEQ ID NO:4360
NT2RP3002790//CTGGAGCCTGATTATGAGAA//SEQ ID NO:4361
NT2RP3002836//CTTTAGCAACATAACCTCCA//SEQ ID NO:4362
NT2RP3002900//TTTCTCCTCCCTAAGACAT//SEQ ID NO:4363
NT2RP3002958//CCCCTCTTCCAGCTCTACAT//SEQ ID NO:4364
NT2RP3002983//AATTTCCTTGCTAGAAGGCT//SEQ ID NO:4365
NT2RP3003354//CGCTCACACCTATTATCCCA//SEQ ID NO:4366
NT2RP3003448//TGTAGTCCCAGCTATTCAGC//SEQ ID NO:4367
NT2RP3003473//AATTAATCTCTCGGTACCAC//SEQ ID NO:4368
NT2RP3003527//TGTCAATGGGCAGGTCGTAG//SEQ ID NO:4369
NT2RP3003532//TAAACTCACTTCCTCTTGGG//SEQ ID NO:4370
NT2RP3003535//CTAATGCCAGTCTTTCAAGA//SEQ ID NO:4371
NT2RP3003559//AATTCTTGTCCTGCTTTTGC//SEQ ID NO:4372
NT2RP3003614//GGGTCTTTGGATTGAGTGTC//SEQ ID NO:4373
NT2RP3003963//CACGATTATCTCTGCCAAAA//SEQ ID NO:4374
NT2RP3004000//TGGCCAGTGTATCAGAGGTC//SEQ ID NO:4375
NT2RP3004025//CACATTCTGGTGGAAAAGCA//SEQ ID NO:4376
NT2RP3004067//TGATCACACGCAGCACTTCC//SEQ ID NO:4377
NT2RP3004075//TTTCAAGTCAACACCTGCAC//SEQ ID NO:4378
NT2RP3004090//TACACTACAGATGGGCAAAA//SEQ ID NO:4379
NT2RP3004119//TCTAAGGCTGGGTACAGTGC//SEQ ID NO:4380
NT2RP3004130//ACATTTCTCCTCCATACGCA//SEQ ID NO:4381
NT2RP3004133//TAACCGCACTATGAGGAAAG//SEQ ID NO:4382

NT2RP3004202//CAGTGCCCTGGTAATAGAGT//SEQ ID NO:4383
NT2RP3004294//ATATTCCACTCCCCATTCGG//SEQ ID NO:4384
NT2RP3004321//GACCAACATGCTAGAAGTGC//SEQ ID NO:4385
NT2RP3004345//AACTCTCATTCCATAACGTG//SEQ ID NO:4386
NT2RP3004406//CACCTAAAAGACTAATCCCT//SEQ ID NO:4387
NT2RP3004552//GAATCCAAAACCCGGTAGGG//SEQ ID NO:4388
NT2RP3004557//GAAAGAGGTCAAAGTACCTG//SEQ ID NO:4389
NT2RP3004625//ATACAGGCAGCAGGAATCAC//SEQ ID NO:4390
NT2RP3004647//CAAGACAACAAAACAGAAGG//SEQ ID NO:4391
NT2RP4000634//ATGAAGAGTTACCTATGTGG//SEQ ID NO:4392
NT2RP4000962//AACCCTGCGGCTTGGAATTCA//SEQ ID NO:4393
NT2RP4001007//TTTCACAATGCTACAGAGGT//SEQ ID NO:4394
NT2RP4001009//AATGTCAGCGGAGCAAAAGA//SEQ ID NO:4395
NT2RP4001467//GTTGAGAATGCTCGACTTGA//SEQ ID NO:4396
NT2RP4001877//AATCATATAGTCCCAGGTTG//SEQ ID NO:4397
NT2RP4001879//GTGTGAGAGTAGTTGGGAA//SEQ ID NO:4398
NT2RP4002187//TCAATAGCTACCTGTAGAGT//SEQ ID NO:4399
NT2RP4002451//CATAAACAGTGACAGCAGAA//SEQ ID NO:4400
NT2RP4002715//AGCAAGGCAATGAGGATACT//SEQ ID NO:4401
NT2RP4002750//CAGCATTTAGGTGTGACGAT//SEQ ID NO:4402
PLACE1000040//ACATTGCTTGAGTCTTGCCA//SEQ ID NO:4403
PLACE1000986//CAAGGAGCTAATAGGGAGAT//SEQ ID NO:4404
PLACE1002080//CTCACTCTGTCATCGAGCCT//SEQ ID NO:4405
PLACE1002547//GTACCCCTAGTGAAGACCTG//SEQ ID NO:4406
PLACE1002911//CAAAGGCAAGTGTTCAGGCT//SEQ ID NO:4407
PLACE1003407//GACTACAAAACCCTGGAAAG//SEQ ID NO:4408
PLACE1003573//GGTGGCATGTAAATAAGACT//SEQ ID NO:4409
PLACE1004078//CTCACCCTTCCAAGTAGCAG//SEQ ID NO:4410
PLACE1004199//GGAATCTGGGAGTCAAAATC//SEQ ID NO:4411
PLACE1004305//GCACCACTTTCGTCTTGAGG//SEQ ID NO:4412
PLACE1004450//GGCACTTAGCTTCTTGTTTT//SEQ ID NO:4413
PLACE1004492//TGGGCATCAATAAACACCTC//SEQ ID NO:4414
PLACE1004630//TGCTTTGTATGGCCTGGGA//SEQ ID NO:4415
PLACE1004816//ATGTGCACACGCAAGCAGAG//SEQ ID NO:4416
PLACE1005031//GGTGTTCCCCTTCTTGTTG//SEQ ID NO:4417
PLACE1005539//AGAGGTAGAATGAGGGGAAA//SEQ ID NO:4418
PLACE1005569//CTGAACCCTGGCCTGTGAAA//SEQ ID NO:4419
PLACE1005601//AGATGGGGACTATGAAGAGG//SEQ ID NO:4420
PLACE1005736//CCTGTAATCCCAGCACTTTG//SEQ ID NO:4421

PLACE1005815//AGAGACAGAGTTTTCCTCTT//SEQ ID NO:4422
PLACE1005927//GGTGTAGCCCATTGTAGAGG//SEQ ID NO:4423
PLACE1006071//TTTGCTCTTTAACTCTGCCT//SEQ ID NO:4424
PLACE1006073//TAAAGGCAGGGTGGAGGAA//SEQ ID NO:4425
PLACE1006079//TGATGTCCACTGTCTTATTG//SEQ ID NO:4426
PLACE1006786//CAAGGAGGTAATAGCGAGAT//SEQ ID NO:4427
PLACE1007077//ATGTGCTGGTAAGTGAAATC//SEQ ID NO:4428
PLACE1007081//GCCGGCCAAGTTTACACGAA//SEQ ID NO:4429
PLACE1007845//TAACCCCACTATGAGGAAG//SEQ ID NO:4430
PLACE1007971//GACAATTCAACTGGAAGACC//SEQ ID NO:4431
PLACE1008282//CGTGATGACTGCCAACTCCA//SEQ ID NO:4432
PLACE1008359//AACAGGGTCCCATTTATTTG//SEQ ID NO:4433
PLACE1008469//TTGTCATCCTCCTGCCTCTG//SEQ ID NO:4434
PLACE1008657//CTCAGCCTTCCAAGTAGCAG//SEQ ID NO:4435
PLACE1008744//TAAACAAGACCCAGCACCAT//SEQ ID NO:4436
PLACE1008984//TCGAGACCGCTTCCCATAGA//SEQ ID NO:4437
PLACE1009546//AGGTACCCGATGACAAGCC//SEQ ID NO:4438
PLACE1010011//GGATATAAAGACAAGGATGC//SEQ ID NO:4439
PLACE1010713//TCAATAGCTACCTGTAGAGT//SEQ ID NO:4440
PLACE1011019//AACGAGTGAAGCTCCATGCC//SEQ ID NO:4441
PLACE1011116//CCATTACAAACCCTTTAACC//SEQ ID NO:4442
PLACE1011181//TGTTATCCATTGTTCACCTG//SEQ ID NO:4443
PLACE1011364//TGTTGACGCTGATTTAGGCA//SEQ ID NO:4444
PLACE3000213//TAAACAAGACCCAGCACCAT//SEQ ID NO:4445
PLACE4000354//TAAACAAGACCCAGCACCAT//SEQ ID NO:4446
PLACE4000455//CAAGGAGGTAATAGCGAGAT//SEQ ID NO:4447
SKNMC1000014//CGAGACAGGGTCTTGGTTTG//SEQ ID NO:4448
SKNMC1000082//TTTCCTTCGGCTGGTATCGC//SEQ ID NO:4449
Y79AA1000030//TCCTACGTTGTGGTGCAGTG//SEQ ID NO:4450
Y79AA1000037//AGCACCCCTTATTGCAAGAT//SEQ ID NO:4451
Y79AA1000127//GATGGTTACTCCTCTTTGGT//SEQ ID NO:4452
Y79AA1000226//TGCTGATGCCTCTGTCCCT//SEQ ID NO:4453
Y79AA1000270//GAAACAACCAAGCACCCCAT//SEQ ID NO:4454
Y79AA1000750//ATAAGGGCAGCTGCGAAGTG//SEQ ID NO:4455
Y79AA1000776//TGTTACTAGCAGCACGAAGC//SEQ ID NO:4456
Y79AA1000777//ACAGAGTTCAGTCCCCTTTA//SEQ ID NO:4457
Y79AA1000876//GTTACAGCACACTGCGATCA//SEQ ID NO:4458
Y79AA1000888//ACTGACTTGAGCAATAAGCC//SEQ ID NO:4459
Y79AA1000959//AGAGTGAGACCATGGGAGGT//SEQ ID NO:4460

Y79AA1000967//GGCACAGACACCATCCTTGA//SEQ ID NO:4461
Y79AA1001056//ACAAATGAGCCTGAAAAGTC//SEQ ID NO:4462
Y79AA1001062//TCGTCCTCACTGCCTTCAAA//SEQ ID NO:4463
Y79AA1001090//AGTGCCCTCAAAGCTCCAGT//SEQ ID NO:4464
Y79AA1001212//ACCAAAGCACTCAAATGTCA//SEQ ID NO:4465
Y79AA1001272//GAATGAAATGTCGTTGAGCA//SEQ ID NO:4466
Y79AA1001426//AATGATTCGCGGCAGCAGGA//SEQ ID NO:4467
Y79AA1001427//GAGAGAGACACACACAGAAA//SEQ ID NO:4468
Y79AA1001523//AGTTTTATACCAGCATTGCC//SEQ ID NO:4469
Y79AA1001530//GGTGTAGAAGTAAAATGGGA//SEQ ID NO:4470
Y79AA1001592//CATTGTGTTCTCTTACTCCT//SEQ ID NO:4471
Y79AA1001727//GCTCCACCTGACGTTCTTTA//SEQ ID NO:4472
Y79AA1001795//GTCTCCCATATCGCTGTCTT//SEQ ID NO:4473
Y79AA1001803//CACTTTCTAATAACCCTTGG//SEQ ID NO:4474
Y79AA1001863//TTGGGATTGGAAACCGCATT//SEQ ID NO:4475
Y79AA1001874//AGAAACCACTGAGGCCCAAG//SEQ ID NO:4476
Y79AA1002058//CAGAAGCAGAAGCAGGAGCA//SEQ ID NO:4477
Y79AA1002121//ATTTACTGCGATTTCTCCTG//SEQ ID NO:4478
Y79AA1002129//GAGTTTCTTTGCTACTTCCA//SEQ ID NO:4479
Y79AA1002334//ATATTTGTGTTTGCCTTGGG//SEQ ID NO:4480
Y79AA1002373//CGATGGCTGGGTCAAATGGT//SEQ ID NO:4481
Y79AA1002376//AATCATGGCTAGGGTGACTT//SEQ ID NO:4482
Y79AA1002378//TCTTCCCACATTCGTTACAC//SEQ ID NO:4483
Y79AA1002381//AGGGAGTACATGTTGGTAAA//SEQ ID NO:4484

[0279] The result of expression frequency analysis is shown in Table 367. Only clones with correlation coefficient of 0.9 or higher are indicated in this Table. Clones that are not presented in the Table include clones for which the assay could not performed because of low expression levels thereof in internal standard samples or because of unexpectedly smaller or larger sizes of the PCR products.

[0280] Among the clones that could be analyzed, clones of which expression levels increased by two fold in response to the IL-1. stimulation 1 or 7 hours after the stimulation are: NT2RM2000514, NT2RP3001159, MAMMA1001237 and MAMMA1000614.

[0281] Clones of which expression levels increased by two fold in response to the TNF-stimulation 1, 3 or 7 hours after the stimulation are:

NT2RM2000582, NT2RM2002109, NT2RP1000679, NT2RP2003664, NT2RP2005597, NT2RP2004108, NT2RP3001592, NT2RP3002738, NT2RP3004133, NT2RP3004321, NT2RP3004557, NT2RP3004294, MAMMA1001237, MAMMA1000141, MAMMA1000788, MAMMA1002070, PLACE1002547, PLACE1003573, PLACE1004305, PLACE1008744, PLACE1011181, PLACE1010713, PLACE1010011, Y79AA1000776, Y79AA1002129,

[0282] Among the clones of which expression levels increased in response to IL-1. stimulation, MAMMA1001237 was a clone of which expression level was varied in response to TNF-. stimulation. Among clones showing higher expression levels (with relative value of 5 or higher) prior to the stimulation, PLACE1002080 is an example of clones

of which expression was suppressed by the stimulation. The expression of the clone decreased by three or more fold in response to the stimulation. These genes were found to be associated with inflammatory reaction induced by IL-1. or TNF-..

[0283] In Example 15, the genes of which expression levels were varied by culturing in the presence of TNF-. were analyzed by hybridization with high-density DNA filter. As for 3 clones (NT2RP3004557, NT2RP3004294 and PLACE 1002547), the results obtained by ATAC-PCR method were similar to those obtained by hybridization method. However, the results obtained by ATAC-PCR method were not necessarily consistent with those obtained by the hybridization method. Possible reasons for the inconsistency are the difference in cells used between the two experiments, unavailability of some data in the ATAC-PCR experiment, and the difference in the method of data treatment.

Table 28

Expression of each cDNA in human tissues (The Table also contains clones with no description in Examples)

Table 185

Expression of each cDNA in human pulmonary arterial endothelial cells cultured in a medium containing bovine serum albumin, glycated bovine serum albumin or advanced glycation endproduct of bovine serum albumin (This table also contains clones without description in Examples).

In the table, EC_G_B/EC_BSA and EC_A_B/EC_BSA represent the ratios EC_glycated_BSA/EC_BSA and EC_AGE_BSA/EC_BSA, respectively.

Clone_name	EC_glycated_BSA	EC_BSA	EC_AGE_BSA	EC_G_B /EC_BSA	EC_A_B /EC_BSA
GAPDH(Cr1)	100.81	134.21	115.16	1.33	1.14
βactin(Cr2)	1101 9	1092 57	997.36	0 99	0.91
ADRGL1000005	26.88	38.27	36.13	1	1
ADRGL1000007	117.89	127.25	133.21	1.08	1.13
ADRGL1000009	29.18	25.65	26.05	1	1
ADRGL1000011	88.9	117.33	142.9	1.32	1.61
ADRGL1000027	33.24	40.53	43.02	1.01	1.08
ADRGL1000058	153.41	208.84	180.05	1.36	1.17
ADRGL1000069	16.8	21.77	29.81	1	1
ADRGL1000077	25.74	24.72	32.86	1	1
ADRGL1000092	84.52	84.15	121.76	1	1.44
ADRGL1000099	76.19	91.53	106.01	1.2	1.39
ADRGL1000136	52.34	44.76	63.06	0.86	1.2
ADRGL1000147	46.08	45.18	52.15	0.98	1.13
ADRGL1000159	31.52	40.24	42.72	1.01	1.07
ADRGL1000160	52.34	60.37	62.29	1.15	1.19
ADRGL1000171	21.46	16.78	25.59	1	1
ADRGL1000181	37.44	45.71	43.65	1.14	1.09
BGGI11000015	52.42	71	65.47	1.35	1.25
BGGI11000016	127.44	122.93	147.57	0.96	1.16
BGGI11000017	25.65	25.74	31.33	1	1
BGGI11000022	32.82	35.19	25.56	1	1
BGGI11000031	44.42	43.8	40.25	0.99	0.91
BGGI11000042	120.38	146.44	165.42	1.22	1.37
BGGI11000046	74.72	58.85	84.95	0.79	1.14
BNGH41000020	4286.08	3584.67	4330.96	0.84	1.01
BNGH41000025	216.67	223.74	257.06	1.03	1.19
BNGH41000026	25.76	28.16	35.52	1	1
BNGH41000027	29.23	23.83	17.86	1	1
BNGH41000035	280.32	238.34	305.66	0.85	1.09
BNGH41000037	59.14	54.86	54.58	0.93	0.92
BNGH41000042	356.1	324.08	411.07	0.91	1.15
BNGH41000048	1201.37	869.03	739.91	0.72	0.62
BNGH41000056	33.94	31.4	40.01	1	1
BNGH41000087	77.58	81.76	91.07	1.05	1.17
BNGH41000091	21.05	21.23	26.82	1	1
BNGH41000157	81.11	57.28	77.46	0.71	0.95
BNGH41000169	21.1	17.59	22.53	1	1
BNGH41000181	63.54	56.92	70.08	0.9	1.1
BNGH41000198	32.53	26.38	34.37	1	1

Y79AA1002373	43.96	55.06	28.34	1.25	0.91
Y79AA1002376	3080.78	3824.05	4481.1	1.24	1.45
Y79AA1002378	73.33	93.61	68.22	1.28	0.93
Y79AA1002381	248.36	288.51	304.13	1.16	1.22
Y79AA1002388	118.82	135.82	129.37	1.14	1.09
Y79AA1002399	36.12	30.1	32.87	1	1
Y79AA1002407	57.84	42.82	52.54	0.74	0.91
Y79AA1002413	78.77	81.36	87.31	1.03	1.11
Y79AA1002416	34.3	30.2	51.99	1	1.3
Y79AA1002429	67.91	69.81	80.19	1.03	1.18
Y79AA1002431	24.66	21.16	23.98	1	1
Y79AA1002433	27.12	18.11	23.63	1	1
Y79AA1002445	78.66	54.58	73.75	0.69	0.94
Y79AA1002461	29.04	24.84	32	1	1
Y79AA1002466	882.69	904.65	782.53	1.02	0.89
Y79AA1002471	53.74	51.26	68.91	0.95	1.28
Y79AA1002472	121.95	127.4	127.11	1.04	1.04
Y79AA1002474	53.33	40.85	47.18	0.77	0.88
Y79AA1002482	103.36	111.11	116.07	1.07	1.12
Y79AA1002487	30.92	25.8	32.51	1	1
Y79AA1002490	101.4	90.92	90.54	0.9	0.89
Y79AA1002493	107.88	125.54	105.75	1.16	0.98
ZRV6C1006278	46.63	30.08	32.23	0.86	0.86

Table 186

Expression of each cDNA in undifferentiated NT2 cells, in NT2 cells cultured in the presence of retinoic acid, or in NT2 cells that were cultured in the presence of retinoic acid and then further cultured in the presence of cell-division inhibitor added (This table also contains clones without description in Examples)

In the table, NT2, NT2_RA, and NT2_RA_INHIB represent untreated NT2 cells, retinoic acid-treated NT2 cells, and retinoic acid/inhibitor-treated NT2 cells, respectively. The assay was performed in triplicate (n=3), and each result was shown in the column of exp.1, exp.2, or exp.3. In addition, "t-test N/R" and "t-test N/I" represent results of test for significance of difference between the untreated cells and the retinoic acid-treated cells, and between the untreated cells and the retinoic acid/inhibitor-treated cells, respectively. The results of the test

HEMBA1003442	4.37	4.67	4.94	3.54	6.73	5.96	
HEMBA1003447	7.55	9.08	49.72	65.41	63.46	65.15	* +
HEMBA1003453	21.03	22.03	42.15	27.85	29.02	27.64	
HEMBA1003461	1.5	2.13	3.49	2.6	3.63	2.2	
HEMBA1003463	2.82	3.68	6.02	5.97	3.84	6.41	
HEMBA1003465	1.77	2.21	6.31	4.75	5.02	3.82	
HEMBA1003480	2.58	3.91	8.62	9.63	9.6	9.42	
HEMBA1003485	7.06	4.84	5.29	6.13	7.26	5.52	
HEMBA1003487	1.8	1.85	3.4	7.12	6.39	6.79	** +
HEMBA1003492	1.42	1.95	4.11	2.41	5.87	2.1	
HEMBA1003494	9.36	8.61	12.16	18.24	18.69	17.83	** +
HEMBA1003497	2.19	2.16	3.29	3.35	6.06	2.97	
HEMBA1003503	0.98	1.74	3.37	5.04	3.18	2.13	
HEMBA1003511	0.99	2.19	3.7	2.3	4.42	2.5	
HEMBA1003528	3.33	4	6.51	5.77	5.04	4.46	
HEMBA1003530	1.33	0.85	3.62	1.97	3.15	2.45	
HEMBA1003531	1.14	1.72	5.39	4.74	7.24	4.51	
HEMBA1003532	12.97	14.66	34.3	28.69	25.31	31.26	
HEMBA1003538	2.54	2.4	17.88	14.54	21.58	16.83	
HEMBA1003545	0.68	2.08	3.17	1.85	3.6	2.17	
HEMBA1003546	1.27	2.03	1.68	1.98	2.15	2.42	
HEMBA1003548	1.4	3.18	3.6	1.41	4.15	2.23	
HEMBA1003553	31.29	31.45	47.99	54.36	41.34	45.65	
HEMBA1003555	1.39	2.73	4.82	3.53	4.48	5.19	
HEMBA1003556	1.24	1.76	2.96	3.14	5.75	3.31	
HEMBA1003560	1.89	2.66	7.87	10.08	13.24	9.9	* +
HEMBA1003565	54.27	66.88	96.28	121.29	139.88	148.68	* +
HEMBA1003568	1.86	2.27	3.24	2.36	7.41	2.78	
HEMBA1003569	2.93	2.61	2.96	5.07	3.95	4.53	** +
HEMBA1003571	3.53	2.33	3.8	5.19	5.3	5.83	* +
HEMBA1003579	3.51	4.29	4.83	3.79	5.68	5.91	
HEMBA1003580	3.82	4.09	4.96	3.11	4.41	3.53	
HEMBA1003581	0.82	2.62	2.07	1.63	3.19	2.4	
HEMBA1003591	10.8	11.44	30.24	33.74	35.7	36.88	* +
HEMBA1003595	0.93	1.16	2.45	2.98	4.02	2.01	
HEMBA1003597	3.15	3.18	8.74	10.82	11.39	11.59	* +
HEMBA1003598	0.58	0.93	1.33	2.62	1.83	1.61	* +
HEMBA1003600	3.71	4.19	13.35	14.77	13.86	16.69	
HEMBA1003602	2.84	2.64	4.89	5.89	6.97	9.14	* +
HEMBA1003604	2.3	3.35	5.67	6.63	8.29	8.16	* +
HEMBA1003610	2.33	3.2	4.48	6.12	5.64	6.81	* +
HEMBA1003615	1.76	2.61	5.23	4.95	5.21	4.96	
HEMBA1003617	3.59	3.54	8.59	6.92	11.37	8.5	
HEMBA1003620	5.76	6.01	4.98	13.48	17.69	12.58	** +
HEMBA1003621	1.6	1.66	3.19	4.52	5.42	5.08	** +
HEMBA1003622	0.96	0.69	1.38	1.47	3.17	2.25	
HEMBA1003630	0.78	1.02	1.95	1.68	2.97	1.55	
HEMBA1003637	0.66	1.93	2.59	2.11	3.11	2.63	
HEMBA1003640	2.33	2.1	5.27	4.16	5.68	5.5	
HEMBA1003645	1.12	1.2	4.41	2.3	3.82	3.06	
HEMBA1003646	0.94	1.21	1.76	1.25	3.25	1.8	
HEMBA1003647	0.49	2.15	3.27	2.46	3.79	2.21	

Table 367

Difference in the expression level of each clone in response to TNF. stimulation or IL-1. stimulation

Before stimulation, IL1 1h, and IL1 7h represent relative levels of expression in the absence of the stimulation, 1 hour after the IL-1. stimulation, and 7 hours after the stimulation, respectively. TNF 1h, TNF 3h, and TNF 7h represent relative levels of expression 1 hour after the TNF. stimulation, 3 hours after the stimulation, and 7 hours after the stimulation, respectively. Correlation coefficients 1 and 2 indicate the correlation coefficients in the calibration curves prepared based on the data for the internal standard in reaction systems A and B, respectively.

Clone	IL1	TNF			Correlation coefficients	
	before stimulation	1h	3h	7h	1	2
NT2RM1000858	5.6	7.6	3.8	4.7	2.1	1.7	0.98	0.94
NT2RM1000462	0.9	0.9	0.5	0.7	0.1	0	1	1
NT2RM1000855	1	1.3	1	1.1	0.4	0.4	1	1
NT2RM1000789	1	0.9	0.4	1	0.4	0.6	0.96	0.98
NT2RM2000306	0.7	1.1	0.3	1.1	0.3	0.1	1	0.98
NT2RM2000514	0.2	0.2	0.6	0.2	0.1	0.2	0.98	0.96
NT2RM2001126	0.5	0	0.4	0.3	0.3	1.2	0.99	0.99
NT2RM2001902	1.3	1.6	0.6	1.3	0.8	0.8	1	1
NT2RM2001738	1.6	1.8	1.5	1.7	0.8	0.9	0.98	1
NT2RM2000582	0.2	0.1	0	0.7	0.1	0.1	0.99	0.99
NT2RM2000773	1.1	1.2	1.4	2	1	0.8	0.95	1
NT2RM2001626	0.4	0.2	0.6	0.7	0.1	0.7	1	1
NT2RM2001643	1.6	3.1	1.2	2.4	0.7	0.8	1	1
NT2RM2001792	0.2	0	0	0.3	0.1	0.1	0.98	0.97
NT2RM2000589	0.2	0.1	0	0.1	0	0	1	0.99
NT2RM2000588	0.6	0.7	0.1	0.8	0.2	0.2	1	1
NT2RM2002109	0	0	0	0.2	0.1	0	0.99	0.99
NT2RM4000284	6.5	9.1	4.8	10.1	3.4	3	1	1
NT2RM4001735	3.8	4.6	2.1	5	1.6	1.4	1	1
NT2RM4000100	0.5	0.6	0.2	0.5	0.3	0.3	0.95	0.95
NT2RM4000417	0.2	0	0	0.2	0.1	0	0.99	0.98
NT2RM4000761	3.2	3.2	2.2	2.6	0.7	0.7	0.95	1
NT2RM4001843	1.5	1.8	1.7	2.8	1.2	0.6	0.98	1
NT2RP1000239	2.1	3.2	1.2	2.1	0.5	0.6	1	0.99
NT2RP1000465	0.9	0.3	0.3	0.9	0.2	0.1	0.97	0.96
NT2RP1000679	0.3	0.3	0.4	0.9	0.2	0.3	0.97	1
NT2RP1001031	1.4	1.4	0.4	1.2	0.1	0.3	1	0.98
NT2RP2001200	2	1.5	0.8	2.2	0.7	0.7	0.99	1
NT2RP2001562	2.7	2.4	0.7	3.5	0.4	1.1	1	0.94
NT2RP2001948	1.1	1.5	0.7	1.3	0.6	0.7	0.97	0.99
NT2RP2002015	1.3	1.7	0.7	1.8	0.6	0.5	0.99	1
NT2RP2003390	2	1.7	1.3	2.3	0.6	0.5	0.99	0.99
NT2RP2003664	0.4	0.1	0.1	0.8	0.1	0	0.99	0.99
NT2RP2005597	1.2	1.4	0.5	2.7	2.2	2.2	0.96	0.99
NT2RP2001469	1.7	1.4	1.2	2	0.6	0.6	1	1
NT2RP2000240	0.9	0.9	0.3	1.4	0.7	0.3	1	1
NT2RP2000610	2.4	2.2	2.1	2.7	1.5	1.6	0.93	0.96

NT2RP2001276	1	0.4	0.4	0.8	0.2	0.7	0.95	1	
NT2RP2001817	1.2	0.8	0.5	1.9	0.7	0.7	1	1	
NT2RP2004069	0.6	0.6	0.4	0.8	0.5	0.3	0.93	0.97	
NT2RP2004108	0.3	0.2	0.6	1.1	0.4	0.5	0.96	1	
NT2RP2005391	0.7	0.5	0.1	1.2	0.3	0.3	1	0.99	
NT2RP2006092	1.6	1.2	0.9	2.1	0.6	0.7	0.97	1	
NT2RP2006134	1.2	1.5	0.7	1.9	1	0	0.91	1	
NT2RP2000818	0.9	0.3	0.3	1.6	0.3	0.3	0.95	1	
NT2RP2000092	1.8	1.8	0.8	2	1	1	0.99	0.98	
NT2RP2000092	1.1	1.1	0.5	1.4	0.6	0.6	0.99	0.97	
NT2RP2001538	2.1	1.9	1.8	2.5	0.6	0.8	0.98	1	
NT2RP2006476	2.1	2.2	1.4	3.2	1.6	2	0.97	0.98	
NT2RP3000616	0.1	0.1	0	0	0	0	1	1	
NT2RP3000721	2.2	2.8	0.7	2.4	0.4	0.4	1	0.98	
NT2RP3001044	1.5	1.9	0.6	2	0.7	0.4	1	1	
NT2RP3001240	0.8	1	0.8	1.5	0.6	0.7	0.97	0.99	
NT2RP3001592	0.3	0.8	0.8	1.1	0	0	0.94	0.93	
NT2RP3002448	4.6	4.2	2.5	4.5	0.8	1.2	1	0.98	
NT2RP3002721	1.3	1.6	0.5	1.4	0.3	0.3	1	0.99	
NT2RP3002738	0.1	0	0.1	1.9	0.1	0.1	0.99	1	
NT2RP3002790	1.6	2	0.6	1.7	0.6	0.5	0.98	1	
NT2RP3002836	1.7	3	0.9	2.4	1.6	0.7	1	1	
NT2RP3003354	0.9	0.7	0.5	0.6	0.4	0.5	0.99	0.92	
NT2RP3003614	0.5	0.4	0	0.3	0.3	0.2	0.99	0.99	
NT2RP3004075	0.8	1.4	0.7	1	0.4	0.4	1	1	
NT2RP3004130	0.3	0.4	0	0.2	0.1	0	0.93	0.96	
NT2RP3004133	1.9	3.5	0.6	3.8	1	1.3	0.99	1	
NT2RP3004321	0.2	0.2	0	1.4	0.4	0.2	1	0.99	
NT2RP3004406	1.3	0.2	0.2	0.7	0.1	0	1	1	
NT2RP3004552	0.1	0.1	0.1	0.1	0	0	1	1	
NT2RP3004557	1.3	1.1	2.2	2.6	1.5	1.4	0.98	0.94	
NT2RP3004647	1.2	2.1	0.6	1.2	1	0.5	1	1	
NT2RP3000201	2.3	2.9	0.4	1	1.3	0.5	1	0.98	
NT2RP3000820	1.2	1.6	0.9	1.2	0.6	0.5	1	1	
NT2RP3000818	1.4	1.5	0.7	1.8	0.5	0.7	1	0.99	
NT2RP3001159	1.2	2.5	1.2	1.4	0.6	0.7	0.99	0.99	
NT2RP3002281	1.6	2	1.2	1.8	1	1.2	0.99	1	
NT2RP3002571	3.9	1.8	1.2	5.2	1.4	0.8	0.99	0.97	
NT2RP3002983	1.4	1.7	0.5	1.4	0.4	0.3	1	1	
NT2RP3003473	0.8	0.9	1	0.7	0.4	0.5	1	0.99	
NT2RP3001976	0.6	1.1	0.1	0.7	0.4	0.1	1	0.99	
NT2RP3002286	1.4	1.8	1	1.6	0.6	0.5	1	0.99	
NT2RP3002353	7.7	6.4	2.2	8.7	1.1	1.3	0.94	0.99	
NT2RP3004025	1.9	2	1	2.1	1	1	0.96	0.98	
NT2RP3004119	0.8	1.1	0.4	0	0	0.2	1	0.99	
NT2RP3000171	0.7	1.3	0.6	1	0.4	0.3	0.99	1	
NT2RP3000676	1.2	1.9	0.7	1.1	1.3	0.5	0.99	1	
NT2RP3000921	0.2	0.1	0	0.2	0.1	0	1	0.99	
NT2RP3002015	0.8	0.6	0.4	0.7	0.1	0.1	0.99	0.99	
NT2RP3004294	0	0	0	0.1	0.1	0	1	1	
NT2RP3004345	0.6	0.4	0.2	0.9	0.2	0.5	1	1	
NT2RP3000148	1.7	2.5	0.8	2	0.8	0.8	1	1	

NT2RP3000232	0.6	0.8	0.4	0.3	0	0	1	0.99	
NT2RP3001650	2.3	1.5	1.6	1.7	1	1.3	1	1	
NT2RP3002411	0.5	0.4	0.1	0.5	0.2	0.1	1	1	
NT2RP4001001	0.8	1.3	0.7	1	0.7	0.4	0.97	0.97	
NT2RP4001877	1.5	0.9	1.1	1.2	0.5	0.7	1	0.99	
NT2RP4002451	0.7	1	0.6	0.7	0.2	0.3	0.91	0.95	
NT2RP4000634	1	1	0.3	0.9	0.3	0.4	0.99	1	
NT2RP4002187	0.4	0.4	0.1	0.7	0.3	0.2	1	0.99	
NT2RP4002715	1.5	1.6	0.7	1.5	0.4	0.3	1	0.99	
MAMMA1000986	3.9	4.1	1.9	4.2	1.8	1.4	0.99	1	
MAMMA1001237	0	0	1.6	0.2	0	0	0.99	0.98	
MAMMA1001978	3.5	3.4	2.3	6	3.4	2.5	0.97	0.98	
MAMMA1002080	0.4	0	0	0.4	0.1	0	1	0.99	
MAMMA1002234	4	4.4	3	7.7	1.9	3	0.97	1	
MAMMA1000614	4.8	1	15.5	5.6	3.9	4.8	0.95	0.93	
MAMMA1000141	7.1	11.5	3.5	14.8	6.5	3.7	1	0.98	
MAMMA1000706	7.2	9.3	3.9	3.7	2.3	2.6	0.98	0.99	
MAMMA1000788	3	3.8	2.8	8.9	4.8	4.2	0.92	0.98	
MAMMA1000994	0.3	0	0	0.4	0	0	1	1	
MAMMA1001310	4.1	6.1	3.8	8	2.5	3.6	0.99	0.95	
MAMMA1001344	2.7	4.4	2.2	3.2	2.6	2.1	1	0.99	
MAMMA1001957	2.3	2.7	1.9	1.7	1	1.8	0.99	1	
MAMMA1002070	0.1	0.1	0	0.8	0.4	0.2	1	0.99	
MAMMA1002586	1.7	1.6	1.2	1.3	0.4	0.3	0.94	1	
MAMMA1000102	2.1	2.3	1.4	3.3	1.6	1.6	1	1	
MAMMA1001066	2.8	2.6	1.8	5.3	0.7	1.2	1	0.98	
MAMMA1001094	2.3	2.9	2	3.3	2.1	2.5	0.96	0.9	
MAMMA1001609	2	3	1.2	2.7	1.7	2.2	0.99	0.97	
PLACE1002547	2	1.7	1.2	4.1	1.2	2	0.95	1	
PLACE1003573	0	0	0	0.1	0	0	1	0.98	
PLACE1004199	0.1	0.2	0	0	0	0	0.99	0.97	
PLACE1004305	0	0	0	0.3	0	0.2	0.96	0.99	
PLACE1004450	0.9	0.3	0	0.1	0	0	0.98	0.98	
PLACE1005031	0.9	0	0	0.5	0	0	0.98	0.99	
PLACE1007845	0.8	1	0.4	0.4	0.1	0.1	1	0.98	
PLACE1008984	1.4	1.2	0.4	1.9	0.6	0.5	0.98	0.98	
PLACE1011116	2.6	1.5	1.6	1.6	0.3	0.4	1	1	
PLACE1000986	0.6	0.2	0.2	0.3	0.1	0.1	1	0.98	
PLACE1004492	1.9	1.9	1.5	3.3	1	1	1	0.97	
PLACE1005569	2.6	0.4	0	1.1	0.3	0.1	0.98	0.99	
PLACE1005601	1.7	1.3	1	2.3	0.6	0.3	0.93	1	
PLACE1006079	0.6	0.3	0	0.1	0.1	0	0.98	0.99	
PLACE1007077	1.1	0	0	0.3	0.1	0	0.97	0.98	
PLACE1008744	0.4	0.1	0.1	1.1	0.1	0	0.98	1	
PLACE1011181	0.6	0.3	0.5	1.6	0.3	0.5	0.98	0.99	
PLACE1005539	0.4	0	0.2	0.3	0.2	0	1	0.93	
PLACE1008282	1.1	0.7	0.6	1.2	0.4	0.4	0.98	1	
PLACE1010713	0.6	0.7	0	1.4	0.5	0.4	0.99	0.95	
PLACE1010011	1.2	1.4	0.2	2.7	1.5	1.7	1	0.99	
PLACE3000213	1.9	0.2	0.1	0.8	0.1	0	0.99	1	
PLACE1002080	6.7	3.9	0.3	1.7	0.8	0.5	0.95	0.98	
SKNMC1000082	1.3	0.1	1.1	0.7	0	0	1	1	

Y79AA1000127	1.8	1.8	1.1	2.1	0.5	0.6	1	1
Y79AA1000226	1.4	0.8	0.6	0.9	0.3	0.4	0.99	0.99
Y79AA1000776	0.3	0.1	0	1.1	0.3	0.5	0.99	0.99
Y79AA1000876	1.1	1.5	1.2	1.3	0.5	0.8	0.97	1
Y79AA1001056	1.7	1.7	0.8	1.4	0.9	0.7	1	1
Y79AA1000777	3.1	3.1	1.2	3.8	0.7	0.5	0.98	0.99
Y79AA1000030	1	1.3	0.2	1.3	0	0.6	0.98	0.96
Y79AA1001212	1.5	1.2	1	2	0.8	0.5	1	0.99
Y79AA1001427	2.3	3	0.6	2	0.8	0.4	1	1
Y79AA1001530	0.9	0.9	0.5	1.1	0.4	0.4	1	1
Y79AA1001592	0.6	0.2	0	0.7	0	0	0.97	1
Y79AA1001727	0.8	0.4	0.2	0.9	0.2	0.1	1	1
Y79AA1001803	0.1	0	0	0.2	0.1	0	0.97	0.99
Y79AA1002373	0	0	0	0	0	0	0.99	1
Y79AA1002376	0.9	0.1	0	1.2	0.1	0.4	0.98	1
Y79AA1001523	0.5	0.5	0.3	0.6	0.3	0.1	1	0.98
Y79AA1000888	1.1	1	0.7	1.4	0.7	0.5	1	1
Y79AA1002129	0.2	0.2	0.1	0.5	0.2	0.2	0.99	1

[0285] The present invention has provided a total of 830 novel full length cDNA clones. As has not yet proceeded the isolation of full length cDNA within the human, the invention has a large significance. Those proteins such as secretory proteins, membrane proteins, and proteins associated with signal transduction, glycoprotein, and transcription are known to be associated with many diseases. Those genes and proteins associating with diseases are useful for developing medicines as they can be used as a diagnostic marker, or a target for gene therapy or developing medicines that is capable of regulating their expression and activity. Especially, the cDNA clones encoding a secretion protein are extremely important for medicinal industry since the protein itself is expected to be effective as a medicine, and also the gene may have potential to be associating with many diseases. Moreover, those proteins such as membrane proteins, and proteins associated with signal transduction, glycoprotein, transcription, and diseases, and the genes encoding the proteins may be used as a disease marker. These cDNA clones are also important for medicinal industry as they may be effective for treating diseases through the regulation of the expression and activity of their encoded proteins.

Table 368

The names of the representative sequences of the clusters (groups) and the corresponding SEQ IDs.

HRIFA000016a : 1573	HRIFA017855a : 1979
HRIFA000071a : 1574	HRIFA017921a : 1980
HRIFA000116a : 1575	HRIFA018075a : 1981
HRIFA000123a : 1576	HRIFA018092a : 1982
HRIFA000264a : 1577	HRIFA018131a : 1983
HRIFA000284a : 1578	HRIFA018134a : 1984
HRIFA000327a : 1579	HRIFA018238a : 1985
HRIFA000415a : 1580	HRIFA018262a : 1986
HRIFA000432a : 1581	HRIFA018287a : 1987
HRIFA000446a : 1582	HRIFA018447a : 1988
HRIFA000553a : 1583	HRIFA018580a : 1989
HRIFA000564a : 1584	HRIFA018666a : 1990
HRIFA000631a : 1585	HRIFA018688a : 1991

HRIFA000683a : 1586
HRIFA000695a : 1587
HRIFA000776a : 1588
HRIFA000814a : 1589
HRIFA000822a : 1590
HRIFA000845a : 1591
HRIFA000899a : 1592
HRIFA000974a : 1593
HRIFA001099a : 1594
HRIFA001132a : 1595
HRIFA001138a : 1596
HRIFA001179a : 1597
HRIFA001200a : 1598
HRIFA001201a : 1599
HRIFA001337a : 1600
HRIFA001341a : 1601
HRIFA001413a : 1602
HRIFA001439a : 1603
HRIFA001489a : 1604
HRIFA001558a : 1605
HRIFA001712a : 1606
HRIFA001720a : 1607
HRIFA001866a : 1608
HRIFA001942a : 1609
HRIFA001971a : 1610
HRIFA001972a : 1611
HRIFA001975a : 1612
HRIFA001984a : 1613
HRIFA002037a : 1614
HRIFA002063a : 1615
HRIFA002102a : 1616
HRIFA002195a : 1617
HRIFA002284a : 1618
HRIFA002309a : 1619
HRIFA002384a : 1620
HRIFA002503a : 1621
HRIFA002689a : 1622
HRIFA002694a : 1623
HRIFA002743a : 1624
HRIFA002762a : 1625
HRIFA002766a : 1626
HRIFA002787a : 1627
HRIFA002805a : 1628
HRIFA002891a : 1629
HRIFA002919a : 1630
HRIFA002980a : 1631
HRIFA002985a : 1632
HRIFA003055a : 1633
HRIFA003063a : 1634
HRIFA003093a : 1635
HRIFA003169a : 1636
HRIFA003340a : 1637
HRIFA018754a : 1992
HRIFA018794a : 1993
HRIFA018827a : 1994
HRIFA018849a : 1995
HRIFA018870a : 1996
HRIFA018904a : 1997
HRIFA018931a : 1998
HRIFA018993a : 1999
HRIFA019105a : 2000
HRIFA019136a : 2001
HRIFA019175a : 2002
HRIFA019185a : 2003
HRIFA019262a : 2004
HRIFA019412a : 2005
HRIFA019437a : 2006
HRIFA019466a : 2007
HRIFA019490a : 2008
HRIFA019498a : 2009
HRIFA019532a : 2010
HRIFA019651a : 2011
HRIFA019867a : 2012
HRIFA019869a : 2013
HRIFA019958a : 2014
HRIFA019960a : 2015
HRIFA020109a : 2016
HRIFA020144a : 2017
HRIFA020163a : 2018
HRIFA020184a : 2019
HRIFA020272a : 2020
HRIFA020335a : 2021
HRIFA020349a : 2022
HRIFA020453a : 2023
HRIFA020466a : 2024
HRIFA020661a : 2025
HRIFA020693a : 2026
HRIFA020707a : 2027
HRIFA020748a : 2028
HRIFA020862a : 2029
HRIFA020883a : 2030
HRIFA020965a : 2031
HRIFA021007a : 2032
HRIFA021040a : 2033
HRIFA021061a : 2034
HRIFA021069a : 2035
HRIFA021136a : 2036
HRIFA021213a : 2037
HRIFA021224a : 2038
HRIFA021323a : 2039
HRIFA021398a : 2040
HRIFA021399a : 2041
HRIFA021445a : 2042
HRIFA021448a : 2043

HRIFA003357a : 1638
HRIFA003379a : 1639
HRIFA003402a : 1640
HRIFA003504a : 1641
HRIFA003592a : 1642
HRIFA003635a : 1643
HRIFA003640a : 1644
HRIFA003883a : 1645
HRIFA003892a : 1646
HRIFA003946a : 1647
HRIFA004006a : 1648
HRIFA004034a : 1649
HRIFA004112a : 1650
HRIFA004145a : 1651
HRIFA004162a : 1652
HRIFA004401a : 1653
HRIFA004426a : 1654
HRIFA004490a : 1655
HRIFA004523a : 1656
HRIFA004663a : 1657
HRIFA004696a : 1658
HRIFA004714a : 1659
HRIFA004745a : 1660
HRIFA004780a : 1661
HRIFA004852a : 1662
HRIFA004919a : 1663
HRIFA005072a : 1664
HRIFA005102a : 1665
HRIFA005184a : 1666
HRIFA005214a : 1667
HRIFA005231a : 1668
HRIFA005240a : 1669
HRIFA005255a : 1670
HRIFA005271a : 1671
HRIFA005296a : 1672
HRIFA005300a : 1673
HRIFA005356a : 1674
HRIFA005369a : 1675
HRIFA005372a : 1676
HRIFA005392a : 1677
HRIFA005409a : 1678
HRIFA005420a : 1679
HRIFA005438a : 1680
HRIFA005462a : 1681
HRIFA005500a : 1682
HRIFA005540a : 1683
HRIFA005644a : 1684
HRIFA005650a : 1685
HRIFA005702a : 1686
HRIFA005720a : 1687
HRIFA005728a : 1688
HRIFA005732a : 1689
HRIFA021494a : 2044
HRIFA021499a : 2045
HRIFA021543a : 2046
HRIFA021594a : 2047
HRIFA021611a : 2048
HRIFA021620a : 2049
HRIFA021637a : 2050
HRIFA021651a : 2051
HRIFA021754a : 2052
HRIFA021781a : 2053
HRIFA021787a : 2054
HRIFA021794a : 2055
HRIFA021855a : 2056
HRIFA021886a : 2057
HRIFA021906a : 2058
HRIFA021985a : 2059
HRIFA022055a : 2060
HRIFA022065a : 2061
HRIFA022106a : 2062
HRIFA022139a : 2063
HRIFA022156a : 2064
HRIFA022166a : 2065
HRIFA022177a : 2066
HRIFA022182a : 2067
HRIFA022203a : 2068
HRIFA022227a : 2069
HRIFA022234a : 2070
HRIFA022249a : 2071
HRIFA022262a : 2072
HRIFA022265a : 2073
HRIFA022328a : 2074
HRIFA022335a : 2075
HRIFA022348a : 2076
HRIFA022411a : 2077
HRIFA022423a : 2078
HRIFA022462a : 2079
HRIFA022493a : 2080
HRIFA022528a : 2081
HRIFA022546a : 2082
HRIFA022564a : 2083
HRIFA022616a : 2084
HRIFA022671a : 2085
HRIFA022691a : 2086
HRIFA022702a : 2087
HRIFA022707a : 2088
HRIFA022714a : 2089
HRIFA022728a : 2090
HRIFA022729a : 2091
HRIFA022737a : 2092
HRIFA022776a : 2093
HRIFA022782a : 2094
HRIFA022794a : 2095

HRIFA005760a : 1690
HRIFA005781a : 1691
HRIFA005944a : 1692
HRIFA006018a : 1693
HRIFA006183a : 1694
HRIFA006216a : 1695
HRIFA006250a : 1696
HRIFA006298a : 1697
HRIFA006448a : 1698
HRIFA006494a : 1699
HRIFA006510a : 1700
HRIFA006566a : 1701
HRIFA006572a : 1702
HRIFA006586a : 1703
HRIFA006596a : 1704
HRIFA006609a : 1705
HRIFA006633a : 1706
HRIFA006642a : 1707
HRIFA006649a : 1708
HRIFA006667a : 1709
HRIFA006730a : 1710
HRIFA006798a : 1711
HRIFA006926a : 1712
HRIFA007013a : 1713
HRIFA007026a : 1714
HRIFA007032a : 1715
HRIFA007068a : 1716
HRIFA007152a : 1717
HRIFA007219a : 1718
HRIFA007228a : 1719
HRIFA007243a : 1720
HRIFA037838a : 1721
HRIFA007256a : 1722
HRIFA007262a : 1723
HRIFA007352a : 1724
HRIFA007424a : 1725
HRIFA007435a : 1726
HRIFA007463a : 1727
HRIFA007493a : 1728
HRIFA007512a : 1729
HRIFA007532a : 1730
HRIFA007541a : 1731
HRIFA007547a : 1732
HRIFA007565a : 1733
HRIFA007571a : 1734
HRIFA007619a : 1735
HRIFA007659a : 1736
HRIFA007722a : 1737
HRIFA007728a : 1738
HRIFA007745a : 1739
HRIFA007829a : 1740
HRIFA007909a : 1741
HRIFA022865a : 2096
HRIFA022875a : 2097
HRIFA022890a : 2098
HRIFA022895a : 2099
HRIFA022985a : 2100
HRIFA023007a : 2101
HRIFA023048a : 2102
HRIFA023069a : 2103
HRIFA023129a : 2104
HRIFA023154a : 2105
HRIFA023212a : 2106
HRIFA023227a : 2107
HRIFA023257a : 2108
HRIFA023304a : 2109
HRIFA023305a : 2110
HRIFA023434a : 2111
HRIFA023464a : 2112
HRIFA023489a : 2113
HRIFA023521a : 2114
HRIFA023605a : 2115
HRIFA023619a : 2116
HRIFA023634a : 2117
HRIFA023767a : 2118
HRIFA023894a : 2119
HRIFA023923a : 2120
HRIFA024088a : 2121
HRIFA024132a : 2122
HRIFA024185a : 2123
HRIFA024197a : 2124
HRIFA024218a : 2125
HRIFA024255a : 2126
HRIFA024305a : 2127
HRIFA024392a : 2128
HRIFA024423a : 2129
HRIFA024473a : 2130
HRIFA024482a : 2131
HRIFA024504a : 2132
HRIFA024533a : 2133
HRIFA024543a : 2134
HRIFA024554a : 2135
HRIFA024718a : 2136
HRIFA024767a : 2137
HRIFA024841a : 2138
HRIFA024884a : 2139
HRIFA024893a : 2140
HRIFA024921a : 2141
HRIFA024937a : 2142
HRIFA024978a : 2143
HRIFA024994a : 2144
HRIFA025033a : 2145
HRIFA025046a : 2146
HRIFA025125a : 2147

HRIFA007985a : 1742
HRIFA008000a : 1743
HRIFA008099a : 1744
HRIFA008131a : 1745
HRIFA034865a : 1746
HRIFA008186a : 1747
HRIFA008200a : 1748
HRIFA008212a : 1749
HRIFA008252a : 1750
HRIFA008284a : 1751
HRIFA008314a : 1752
HRIFA008362a : 1753
HRIFA008387a : 1754
HRIFA008426a : 1755
HRIFA008459a : 1756
HRIFA008483a : 1757
HRIFA008547a : 1758
HRIFA008596a : 1759
HRIFA008606a : 1760
HRIFA008611a : 1761
HRIFA008661a : 1762
HRIFA008717a : 1763
HRIFA008753a : 1764
HRIFA008784a : 1765
HRIFA008790a : 1766
HRIFA008827a : 1767
HRIFA008949a : 1768
HRIFA008976a : 1769
HRIFA008981a : 1770
HRIFA008989a : 1771
HRIFA009071a : 1772
HRIFA009101a : 1773
HRIFA009123a : 1774
HRIFA009136a : 1775
HRIFA009171a : 1776
HRIFA009214a : 1777
HRIFA009220a : 1778
HRIFA009339a : 1779
HRIFA009372a : 1780
HRIFA009392a : 1781
HRIFA009414a : 1782
HRIFA009451a : 1783
HRIFA009482a : 1784
HRIFA009578a : 1785
HRIFA009762a : 1786
HRIFA009764a : 1787
HRIFA009783a : 1788
HRIFA009825a : 1789
HRIFA009852a : 1790
HRIFA009881a : 1791
HRIFA009983a : 1792
HRIFA010005a : 1793
HRIFA025143a : 2148
HRIFA025250a : 2149
HRIFA025261a : 2150
HRIFA025276a : 2151
HRIFA025290a : 2152
HRIFA025327a : 2153
HRIFA025353a : 2154
HRIFA025360a : 2155
HRIFA025479a : 2156
HRIFA025488a : 2157
HRIFA025492a : 2158
HRIFA025498a : 2159
HRIFA025514a : 2160
HRIFA025636a : 2161
HRIFA025695a : 2162
HRIFA025703a : 2163
HRIFA025706a : 2164
HRIFA025766a : 2165
HRIFA025771a : 2166
HRIFA025778a : 2167
HRIFA025786a : 2168
HRIFA025792a : 2169
HRIFA025800a : 2170
HRIFA025904a : 2171
HRIFA025907a : 2172
HRIFA037340a : 2173
HRIFA025936a : 2174
HRIFA025966a : 2175
HRIFA025978a : 2176
HRIFA026089a : 2177
HRIFA026121a : 2178
HRIFA026151a : 2179
HRIFA026153a : 2180
HRIFA026203a : 2181
HRIFA026210a : 2182
HRIFA026242a : 2183
HRIFA026265a : 2184
HRIFA026303a : 2185
HRIFA026316a : 2186
HRIFA026346a : 2187
HRIFA026351a : 2188
HRIFA026364a : 2189
HRIFA026382a : 2190
HRIFA026465a : 2191
HRIFA026490a : 2192
HRIFA026496a : 2193
HRIFA026519a : 2194
HRIFA026564a : 2195
HRIFA026576a : 2196
HRIFA026615a : 2197
HRIFA026618a : 2198
HRIFA026659a : 2199

HRIFA010034a : 1794
HRIFA010070a : 1795
HRIFA010078a : 1796
HRIFA010085a : 1797
HRIFA010090a : 1798
HRIFA010130a : 1799
HRIFA010152a : 1800
HRIFA010176a : 1801
HRIFA010206a : 1802
HRIFA010301a : 1803
HRIFA010319a : 1804
HRIFA010322a : 1805
HRIFA010361a : 1806
HRIFA010394a : 1807
HRIFA010425a : 1808
HRIFA010460a : 1809
HRIFA010466a : 1810
HRIFA010490a : 1811
HRIFA010593a : 1812
HRIFA010736a : 1813
HRIFA010790a : 1814
HRIFA010799a : 1815
HRIFA010859a : 1816
HRIFA010891a : 1817
HRIFA010942a : 1818
HRIFA010975a : 1819
HRIFA010988a : 1820
HRIFA011016a : 1821
HRIFA011105a : 1822
HRIFA011128a : 1823
HRIFA011179a : 1824
HRIFA011193a : 1825
HRIFA011197a : 1826
HRIFA011347a : 1827
HRIFA011403a : 1828
HRIFA011449a : 1829
HRIFA011484a : 1830
HRIFA011512a : 1831
HRIFA011580a : 1832
HRIFA011659a : 1833
HRIFA011802a : 1834
HRIFA011820a : 1835
HRIFA011926a : 1836
HRIFA011947a : 1837
HRIFA012022a : 1838
HRIFA012069a : 1839
HRIFA012151a : 1840
HRIFA012167a : 1841
HRIFA012278a : 1842
HRIFA012282a : 1843
HRIFA012283a : 1844
HRIFA012290a : 1845
HRIFA026735a : 2200
HRIFA026764a : 2201
HRIFA026789a : 2202
HRIFA026813a : 2203
HRIFA026860a : 2204
HRIFA026889a : 2205
HRIFA026899a : 2206
HRIFA026918a : 2207
HRIFA026923a : 2208
HRIFA027012a : 2209
HRIFA027045a : 2210
HRIFA027125a : 2211
HRIFA027173a : 2212
HRIFA027179a : 2213
HRIFA027187a : 2214
HRIFA027265a : 2215
HRIFA027327a : 2216
HRIFA027329a : 2217
HRIFA027355a : 2218
HRIFA027485a : 2219
HRIFA027493a : 2220
HRIFA027536a : 2221
HRIFA027549a : 2222
HRIFA027619a : 2223
HRIFA027622a : 2224
HRIFA027625a : 2225
HRIFA027644a : 2226
HRIFA027656a : 2227
HRIFA027673a : 2228
HRIFA027681a : 2229
HRIFA027701a : 2230
HRIFA027714a : 2231
HRIFA027717a : 2232
HRIFA027722a : 2233
HRIFA027754a : 2234
HRIFA027803a : 2235
HRIFA027860a : 2236
HRIFA027867a : 2237
HRIFA027874a : 2238
HRIFA027940a : 2239
HRIFA027961a : 2240
HRIFA028061a : 2241
HRIFA028157a : 2242
HRIFA028187a : 2243
HRIFA028262a : 2244
HRIFA028371a : 2245
HRIFA028401a : 2246
HRIFA028402a : 2247
HRIFA028440a : 2248
HRIFA028465a : 2249
HRIFA028468a : 2250
HRIFA028497a : 2251

HRIFA012333a : 1846
HRIFA012354a : 1847
HRIFA012417a : 1848
HRIFA012427a : 1849
HRIFA012436a : 1850
HRIFA012480a : 1851
HRIFA012513a : 1852
HRIFA012515a : 1853
HRIFA012584a : 1854
HRIFA012625a : 1855
HRIFA012692a : 1856
HRIFA012702a : 1857
HRIFA012737a : 1858
HRIFA012761a : 1859
HRIFA012795a : 1860
HRIFA012881a : 1861
HRIFA012885a : 1862
HRIFA012914a : 1863
HRIFA012969a : 1864
HRIFA012990a : 1865
HRIFA012999a : 1866
HRIFA013092a : 1867
HRIFA013103a : 1868
HRIFA013135a : 1869
HRIFA013235a : 1870
HRIFA013254a : 1871
HRIFA013265a : 1872
HRIFA013276a : 1873
HRIFA013279a : 1874
HRIFA013288a : 1875
HRIFA013376a : 1876
HRIFA013477a : 1877
HRIFA013586a : 1878
HRIFA013589a : 1879
HRIFA013620a : 1880
HRIFA013668a : 1881
HRIFA013726a : 1882
HRIFA013744a : 1883
HRIFA013899a : 1884
HRIFA013911a : 1885
HRIFA013919a : 1886
HRIFA013932a : 1887
HRIFA013980a : 1888
HRIFA014006a : 1889
HRIFA014024a : 1890
HRIFA014056a : 1891
HRIFA014111a : 1892
HRIFA014133a : 1893
HRIFA014178a : 1894
HRIFA014185a : 1895
HRIFA014303a : 1896
HRIFA014336a : 1897
HRIFA028501a : 2252
HRIFA028511a : 2253
HRIFA028573a : 2254
HRIFA028576a : 2255
HRIFA028592a : 2256
HRIFA028614a : 2257
HRIFA028651a : 2258
HRIFA028652a : 2259
HRIFA028654a : 2260
HRIFA028708a : 2261
HRIFA028790a : 2262
HRIFA028804a : 2263
HRIFA028867a : 2264
HRIFA028911a : 2265
HRIFA028926a : 2266
HRIFA028983a : 2267
HRIFA029002a : 2268
HRIFA029050a : 2269
HRIFA029107a : 2270
HRIFA029208a : 2271
HRIFA029209a : 2272
HRIFA029256a : 2273
HRIFA029263a : 2274
HRIFA029274a : 2275
HRIFA029278a : 2276
HRIFA029285a : 2277
HRIFA029317a : 2278
HRIFA029327a : 2279
HRIFA029349a : 2280
HRIFA029393a : 2281
HRIFA029398a : 2282
HRIFA029425a : 2283
HRIFA029434a : 2284
HRIFA029440a : 2285
HRIFA029460a : 2286
HRIFA029467a : 2287
HRIFA029508a : 2288
HRIFA029511a : 2289
HRIFA029577a : 2290
HRIFA029602a : 2291
HRIFA029649a : 2292
HRIFA029715a : 2293
HRIFA029730a : 2294
HRIFA029779a : 2295
HRIFA029792a : 2296
HRIFA029802a : 2297
HRIFA029866a : 2298
HRIFA029932a : 2299
HRIFA030025a : 2300
HRIFA030045a : 2301
HRIFA030097a : 2302
HRIFA030103a : 2303

HRIFA014396a : 1898
HRIFA014397a : 1899
HRIFA014417a : 1900
HRIFA014465a : 1901
HRIFA014467a : 1902
HRIFA014482a : 1903
HRIFA014500a : 1904
HRIFA014561a : 1905
HRIFA014568a : 1906
HRIFA014590a : 1907
HRIFA014598a : 1908
HRIFA014620a : 1909
HRIFA014621a : 1910
HRIFA014688a : 1911
HRIFA014692a : 1912
HRIFA014702a : 1913
HRIFA014819a : 1914
HRIFA014868a : 1915
HRIFA014951a : 1916
HRIFA014953a : 1917
HRIFA014967a : 1918
HRIFA015063a : 1919
HRIFA015070a : 1920
HRIFA015122a : 1921
HRIFA015129a : 1922
HRIFA015219a : 1923
HRIFA015236a : 1924
HRIFA015246a : 1925
HRIFA015351a : 1926
HRIFA015409a : 1927
HRIFA015423a : 1928
HRIFA015443a : 1929
HRIFA015453a : 1930
HRIFA015471a : 1931
HRIFA015486a : 1932
HRIFA015506a : 1933
HRIFA015536a : 1934
HRIFA015547a : 1935
HRIFA015568a : 1936
HRIFA015671a : 1937
HRIFA015682a : 1938
HRIFA015756a : 1939
HRIFA015764a : 1940
HRIFA015802a : 1941
HRIFA015811a : 1942
HRIFA015902a : 1943
HRIFA015947a : 1944
HRIFA015995a : 1945
HRIFA016070a : 1946
HRIFA016129a : 1947
HRIFA016214a : 1948
HRIFA016240a : 1949
HRIFA030106a : 2304
HRIFA030147a : 2305
HRIFA030203a : 2306
HRIFA030237a : 2307
HRIFA030248a : 2308
HRIFA030250a : 2309
HRIFA030264a : 2310
HRIFA030342a : 2311
HRIFA030370a : 2312
HRIFA030371a : 2313
HRIFA030381a : 2314
HRIFA030385a : 2315
HRIFA030394a : 2316
HRIFA030408a : 2317
HRIFA030411a : 2318
HRIFA030448a : 2319
HRIFA030456a : 2320
HRIFA030461a : 2321
HRIFA030472a : 2322
HRIFA030509a : 2323
HRIFA030511a : 2324
HRIFA030545a : 2325
HRIFA030566a : 2326
HRIFA030599a : 2327
HRIFA030629a : 2328
HRIFA030642a : 2329
HRIFA030662a : 2330
HRIFA030839a : 2331
HRIFA030981a : 2332
HRIFA031062a : 2333
HRIFA031075a : 2334
HRIFA031091a : 2335
HRIFA031126a : 2336
HRIFA031249a : 2337
HRIFA031336a : 2338
HRIFA031350a : 2339
HRIFA031395a : 2340
HRIFA031397a : 2341
HRIFA031438a : 2342
HRIFA031472a : 2343
HRIFA031510a : 2344
HRIFA031672a : 2345
HRIFA031869a : 2346
HRIFA031871a : 2347
HRIFA031895a : 2348
HRIFA031935a : 2349
HRIFA031986a : 2350
HRIFA032009a : 2351
HRIFA032011a : 2352
HRIFA032066a : 2353
HRIFA032067a : 2354
HRIFA032070a : 2355

HRIFA016255a : 1950
HRIFA016290a : 1951
HRIFA016430a : 1952
HRIFA016599a : 1953
HRIFA016623a : 1954
HRIFA016639a : 1955
HRIFA016654a : 1956
HRIFA016669a : 1957
HRIFA016758a : 1958
HRIFA016838a : 1959
HRIFA016963a : 1960
HRIFA017031a : 1961
HRIFA017146a : 1962
HRIFA017190a : 1963
HRIFA017257a : 1964
HRIFA017295a : 1965
HRIFA017312a : 1966
HRIFA017456a : 1967
HRIFA017457a : 1968
HRIFA017509a : 1969
HRIFA017594a : 1970
HRIFA017643a : 1971
HRIFA017670a : 1972
HRIFA017703a : 1973
HRIFA017729a : 1974
HRIFA017791a : 1975
HRIFA017801a : 1976
HRIFA017818a : 1977
HRIFA017836a : 1978
HRIFA032073a : 2356
HRIFA032079a : 2357
HRIFA032097a : 2358
HRIFA032161a : 2359
HRIFA032186a : 2360
HRIFA032224a : 2361
HRIFA032257a : 2362
HRIFA032271a : 2363
HRIFA032274a : 2364
HRIFA032275a : 2365
HRIFA032360a : 2366
HRIFA032389a : 2367
HRIFA032433a : 2368
HRIFA032453a : 2369
HRIFA032478a : 2370
HRIFA032506a : 2371
HRIFA032511a : 2372
HRIFA032530a : 2373
HRIFA032587a : 2374
HRIFA032605a : 2375
HRIFA032642a : 2376
HRIFA032696a : 2377
HRIFA032730a : 2378
HRIFA032820a : 2379
HRIFA032984a : 2380
HRIFA033349a : 2381
HRIFA033718a : 2382
HRIFA034010a : 2383

Table 369

The names of the internal sequences that are used in the selection of the clones from the representative sequences, and the corresponding SEQ IDs.

AA533598 : 2384	HRIFA036799a : 2463
AI051329 : 2385	HRIFA037138a : 2464
HRIFA000595a : 2386	HRIFA037776a : 2465
HRIFA000667a : 2387	HRIFA037838a : 2466
HRIFA000878a : 2388	HRIRA000001a : 2467
HRIFA001269a : 2389	HRIRA000041a : 2468
HRIFA001283a : 2390	HRIRA000058a : 2469
HRIFA002000a : 2391	HRIRA000260a : 2470
HRIFA002196a : 2392	HRIRA000490a : 2471
HRIFA003583a : 2393	HRIRA000522a : 2472
HRIFA005077a : 2394	HRIRA000553a : 2473
HRIFA005781a : 2395	HRIRA000563a : 2474
HRIFA006216a : 2396	HRIRA000640a : 2475
HRIFA006468a : 2397	HRIRA000725a : 2476
HRIFA006822a : 2398	HRIRA000998a : 2477
HRIFA007048a : 2399	HRIRA001053a : 2478
HRIFA007661a : 2400	HRIRA001314a : 2479

HRIFA007777a : 2401
HRIFA007997a : 2402
HRIFA008312a : 2403
HRIFA009250a : 2404
HRIFA009495a : 2405
HRIFA009607a : 2406
HRIFA009923a : 2407
HRIFA009978a : 2408
HRIFA010730a : 2409
HRIFA011029a : 2410
HRIFA011416a : 2411
HRIFA011461a : 2412
HRIFA012670a : 2413
HRIFA012717a : 2414
HRIFA012802a : 2415
HRIFA013357a : 2416
HRIFA013484a : 2417
HRIFA015333a : 2418
HRIFA015375a : 2419
HRIFA015663a : 2420
HRIFA016287a : 2421
HRIFA016302a : 2422
HRIFA016782a : 2423
HRIFA018555a : 2424
HRIFA019338a : 2425
HRIFA020315a : 2426
HRIFA020806a : 2427
HRIFA022264a : 2428
HRIFA022923a : 2429
HRIFA023027a : 2430
HRIFA023218a : 2431
HRIFA023363a : 2432
HRIFA023434a : 2433
HRIFA023444a : 2434
HRIFA023551a : 2435
HRIFA023558a : 2436
HRIFA023641a : 2437
HRIFA023798a : 2438
HRIFA024330a : 2439
HRIFA024338a : 2440
HRIFA024384a : 2441
HRIFA024644a : 2442
HRIFA025170a : 2443
HRIFA025496a : 2444
HRIFA025565a : 2445
HRIFA025651a : 2446
HRIFA026224a : 2447
HRIFA026729a : 2448
HRIFA026925a : 2449
HRIFA028501a : 2450
HRIFA029454a : 2451
HRIFA030181a : 2452
HRIRA001443a : 2480
HRIRA001473a : 2481
HRIRA001648a : 2482
HRIRA001690a : 2483
HRIRA001726a : 2484
HRIRA001884a : 2485
HRIRA002098a : 2486
HRIRA002100a : 2487
HRIRA002155a : 2488
HRIRA002307a : 2489
HRIRA002442a : 2490
HRIRA002446a : 2491
HRIRA002479a : 2492
HRIRA002945a : 2493
HRIRA003028a : 2494
HRIRA003108a : 2495
HRIRA003139a : 2496
HRIRA003819a : 2497
HRIRA004049a : 2498
HRIRA004286a : 2499
HRIRA004583a : 2500
HRIRA004691a : 2501
HRIRA004783a : 2502
HRIRA005152a : 2503
HRIRA005221a : 2504
HRIRA005227a : 2505
HRIRA005305a : 2506
HRIRA005563a : 2507
HRIRA006263a : 2508
HRIRA006324a : 2509
HRIRA006517a : 2510
HRIRA006580a : 2511
HRIRA007665a : 2512
HRIRA007680a : 2513
HRIRA008129a : 2514
HRIRA008152a : 2515
HRIRA008276a : 2516
HRIRA008329a : 2517
HRIRA008854a : 2518
HRIRA008896a : 2519
HRIRA008958a : 2520
HRIRA009551a : 2521
HRIRA009828a : 2522
HRIRA010472a : 2523
HRIRA012442a : 2524
HRIRA012921a : 2525
HRIRA013325a : 2526
HRIRA013644a : 2527
HRIRA013675a : 2528
HRIRA013702a : 2529
HRIRA013757a : 2530
HRIRA013951a : 2531

HRIFA032701a : 2453	HRIRA014256a : 2532
HRIFA032801a : 2454	HRIRA014380a : 2533
HRIFA033384a : 2455	HRIRA015831a : 2534
HRIFA033682a : 2456	HRIRA015904a : 2535
HRIFA033930a : 2457	HRIRA016124a : 2536
HRIFA034817a : 2458	HRIRA017071a : 2537
HRIFA035409a : 2459	HRIRA018191a : 2538
HRIFA035542a : 2460	HRIRA020304a : 2539
HRIFA035577a : 2461	HRIRA000579a : 2540
HRIFA036630a : 2462	

[0286] The internal sequences include EST, HRIFA(the representative sequence of the 5'-end), and HRIRA (the representative sequence of the 3'-end).

Table 370

clone	the name of full-length nucleotide sequences	SEQ ID NO of the full-length nucleotide sequences	SEQ ID NO of the deduced amino acid sequences
HEMBA1000006	C-HEMBA1000006	2547	2548
nnnnnnnnnnnn	C-nnnnnnnnnnnn	nnnn	nnnn
HEMBA1000121	C-HEMBA1000121	2551	2552
HEMBA1000128	C-HEMBA1000128	2553	2554
HEMBA1000275	C-HEMBA1000275	2555	2556
HEMBA1000300	C-HEMBA1000300	2557	
HEMBA1000349	C-HEMBA1000349	2558	2559
HEMBA1000443	C-HEMBA1000443	2560	2561
HEMBA1000590	C-HEMBA1000590	2562	2563
HEMBA1000634	C-HEMBA1000634	2564	2565
HEMBA1000713	C-HEMBA1000713	2566	2567
HEMBA1000745	C-HEMBA1000745	2568	2569
HEMBA1000907	C-HEMBA1000907	2570	2571
HEMBA1000940	C-HEMBA1000940	2572	2573
HEMBA1000962	C-HEMBA1000962	2574	2575
HEMBA1001221	C-HEMBA1001221	2576	2577
HEMBA1001228	C-HEMBA1001228	2578	2579
HEMBA1001297	C-HEMBA1001297	2580	
HEMBA1001390	C-HEMBA1001390	2581	2582
HEMBA1001563	C-HEMBA1001563	2583	
HEMBA1001621	C-HEMBA1001621	2584	2585
nnnnnnnnnnnn	C-nnnnnnnnnnnn	nnnn	nnnn
HEMBA1001878	C-HEMBA1001878	2588	2589
HEMBA1002131	C-HEMBA1002131	2590	2591
HEMBA1002163	C-HEMBA1002163	2592	2593
HEMBA1002164	C-HEMBA1002164	2594	2595
HEMBA1002167	C-HEMBA1002167	2596	2597
HEMBA1002178	C-HEMBA1002178	2598	2599
nnnnnnnnnnnn	C-nnnnnnnnnnnn	nnnn	nnnn

HEMBA1002195	C-HEMBA1002195	2602	2603
HEMBA1002227	C-HEMBA1002227	2604	2605
HEMBA1002239	C-HEMBA1002239	2606	
HEMBA1002316	C-HEMBA1002316	2607	2608
HEMBA1002420	C-HEMBA1002420	2609	2610
HEMBA1002421	C-HEMBA1002421	2611	2612
HEMBA1002524	C-HEMBA1002524	2613	2614
HEMBA1002551	C-HEMBA1002551	2615	2616
HEMBA1002767	C-HEMBA1002767	2617	2618
HEMBA1002992	C-HEMBA1002992	2619	2620
HEMBA1003047	C-HEMBA1003047	2621	2622
HEMBA1003072	C-HEMBA1003072	2623	2624
HEMBA1003101	C-HEMBA1003101	2625	2626
HEMBA1003230	C-HEMBA1003230	2627	2628
HEMBA1003294	C-HEMBA1003294	2629	
HEMBA1003315	C-HEMBA1003315	2630	2631
HEMBA1003392	C-HEMBA1003392	2632	2633
HEMBA1003399	C-HEMBA1003399	2634	2635
HEMBA1003487	C-HEMBA1003487	2636	2637
HEMBA1003530	C-HEMBA1003530	2638	2639
HEMBA1003602	C-HEMBA1003602	2640	2641
HEMBA1003732	C-HEMBA1003732	2642	2643
HEMBA1003945	C-HEMBA1003945	2644	2645
HEMBA1004110	C-HEMBA1004110	2646	2647
HEMBA1004250	C-HEMBA1004250	2648	2649
HEMBA1004391	C-HEMBA1004391	2650	2651
HEMBA1004444	C-HEMBA1004444	2652	2653
HEMBA1004454	C-HEMBA1004454	2654	2655
HEMBA1004505	C-HEMBA1004505	2656	2657
HEMBA1004797	C-HEMBA1004797	2658	2659
HEMBA1004982	C-HEMBA1004982	2660	2661
HEMBA1005070	C-HEMBA1005070	2662	2663
HEMBA1005084	C-HEMBA1005084	2664	2665
HEMBA1005145	C-HEMBA1005145	2666	2667
HEMBA1005430	C-HEMBA1005430	2668	2669
HEMBA1005449	C-HEMBA1005449	2670	2671
HEMBA1005489	C-HEMBA1005489	2672	2673
HEMBA1005522	C-HEMBA1005522	2674	2675
HEMBA1005545	C-HEMBA1005545	2676	2677
HEMBA1005698	C-HEMBA1005698	2678	2679
HEMBA1005913	C-HEMBA1005913	2680	
HEMBA1005929	C-HEMBA1005929	2681	2682
HEMBA1005945	C-HEMBA1005945	2683	2684
HEMBA1006016	C-HEMBA1006016	2685	
HEMBA1006171	C-HEMBA1006171	2686	2687
HEMBA1006299	C-HEMBA1006299	2688	2689
HEMBA1006311	C-HEMBA1006311	2690	2691
HEMBA1006335	C-HEMBA1006335	2692	2693
HEMBA1006430	C-HEMBA1006430	2694	2695
HEMBA1006482	C-HEMBA1006482	2696	2697
HEMBA1006572	C-HEMBA1006572	2698	2699
HEMBA1006707	C-HEMBA1006707	2700	2701

HEMBA1006724	C-HEMBA1006724	2702	2703
HEMBA1006902	C-HEMBA1006902	2704	2705
HEMBA1006916	C-HEMBA1006916	2706	2707
HEMBA1006960	C-HEMBA1006960	2708	2709
HEMBA1007013	C-HEMBA1007013	2710	2711
HEMBA1007057	C-HEMBA1007057	2712	2713
HEMBA1007241	C-HEMBA1007241	2714	
HEMBA1007291	C-HEMBA1007291	2715	2716
HEMBA1007332	C-HEMBA1007332	2717	
HEMBB1000276	C-HEMBB1000276	2718	
HEMBB1000447	C-HEMBB1000447	2719	2720
HEMBB1000642	C-HEMBB1000642	2721	
HEMBB1000668	C-HEMBB1000668	2722	2723
HEMBB1000679	C-HEMBB1000679	2724	2725
HEMBB1000881	C-HEMBB1000881	2726	2727
HEMBB1000905	C-HEMBB1000905	2728	2729
HEMBB1001026	C-HEMBB1001026	2730	2731
HEMBB1001048	C-HEMBB1001048	2732	2733
HEMBB1001200	C-HEMBB1001200	2734	
HEMBB1001407	C-HEMBB1001407	2735	2736
HEMBB1001530	C-HEMBB1001530	2737	2738
HEMBB1001573	C-HEMBB1001573	2739	2740
nnnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn
HEMBB1001847	C-HEMBB1001847	2743	2744
HEMBB1001978	C-HEMBB1001978	2745	2746
HEMBB1002162	C-HEMBB1002162	2747	2748
HEMBB1002228	C-HEMBB1002228	2749	
HEMBB1002245	C-HEMBB1002245	2750	2751
HEMBB1002427	C-HEMBB1002427	2752	2753
HEMBB1002465	C-HEMBB1002465	2754	2755
HEMBB1002663	C-HEMBB1002663	2756	2757
HEMBB1002693	C-HEMBB1002693	2758	2759
MAMMA1000046	C-MAMMA1000046	2760	
MAMMA1000118	C-MAMMA1000118	2761	2762
nnnnnnnnnnnn	C-nnnnnnnnnnnn	nnnn	nnnn
MAMMA1000449	C-MAMMA1000449	2765	
MAMMA1000457	C-MAMMA1000457	2766	2767
MAMMA1000591	C-MAMMA1000591	2768	2769
MAMMA1000681	C-MAMMA1000681	2770	2771
MAMMA1001043	C-MAMMA1001043	2772	2773
MAMMA1001893	C-MAMMA1001893	2774	2775
NT2RM2000241	C-NT2RM2000241	2776	2777
NT2RM2000306	C-NT2RM2000306	2778	2779
NT2RM2000410	C-NT2RM2000410	2780	2781
NT2RM2000423	C-NT2RM2000423	2782	2783
NT2RM2000497	C-NT2RM2000497	2784	2785
NT2RM2000514	C-NT2RM2000514	2786	2787
NT2RM2000622	C-NT2RM2000622	2788	2789
NT2RM2001126	C-NT2RM2001126	2790	2791
NT2RM2001902	C-NT2RM2001902	2792	2793
NT2RM2001939	C-NT2RM2001939	2794	2795
NT2RM2001941	C-NT2RM2001941	2796	2797

NT2RM4000198	C-NT2RM4000198	2798	2799
NT2RM4000284	C-NT2RM4000284	2800	2801
NT2RM4000295	C-NT2RM4000295	2802	2803
NT2RM4000326	C-NT2RM4000326	2804	2805
NT2RM4000444	C-NT2RM4000444	2806	2807
NT2RM4000587	C-NT2RM4000587	2808	2809
NT2RM4000648	C-NT2RM4000648	2810	2811
NT2RM4000997	C-NT2RM4000997	2812	2813
NT2RM4001321	C-NT2RM4001321	2814	2815
NT2RM4001325	C-NT2RM4001325	2816	2817
NT2RM4001735	C-NT2RM4001735	2818	2819
NT2RM4002352	C-NT2RM4002352	2820	2821
NT2RP1000002	C-NT2RP1000002	2822	2823
NT2RP1000050	C-NT2RP1000050	2824	2825
NT2RP1000181	C-NT2RP1000181	2826	2827
NT2RP1000261	C-NT2RP1000261	2828	2829
NT2RP1000300	C-NT2RP1000300	2830	2831
NT2RP1000325	C-NT2RP1000325	2832	2833
NT2RP1000448	C-NT2RP1000448	2834	2835
NT2RP1000551	C-NT2RP1000551	2836	2837
NT2RP1000579	C-NT2RP1000579	2838	2839
NT2RP1000613	C-NT2RP1000613	2840	2841
NT2RP1000903	C-NT2RP1000903	2842	2843
NT2RP1000981	C-NT2RP1000981	2844	2845
NT2RP1001004	C-NT2RP1001004	2846	2847
NT2RP1001020	C-NT2RP1001020	2848	2849
NT2RP1001563	C-NT2RP1001563	2850	2851
NT2RP2000394	C-NT2RP2000394	2852	2853
NT2RP2000479	C-NT2RP2000479	2854	2855
NT2RP2000514	C-NT2RP2000514	2856	2857
NT2RP2000533	C-NT2RP2000533	2858	2859
NT2RP2000649	C-NT2RP2000649	2860	2861
NT2RP2000663	C-NT2RP2000663	2862	2863
NT2RP2000694	C-NT2RP2000694	2864	2865
NT2RP2000903	C-NT2RP2000903	2866	2867
NT2RP2001480	C-NT2RP2001480	2868	2869
NT2RP2001495	C-NT2RP2001495	2870	2871
NT2RP2001514	C-NT2RP2001514	2872	2873
NT2RP2001529	C-NT2RP2001529	2874	2875
NT2RP2001769	C-NT2RP2001769	2876	2877
NT2RP2001878	C-NT2RP2001878	2878	2879
NT2RP2001903	C-NT2RP2001903	2880	2881
NT2RP2001915	C-NT2RP2001915	2882	2883
NT2RP2001956	C-NT2RP2001956	2884	2885
NT2RP2002063	C-NT2RP2002063	2886	2887
NT2RP2002188	C-NT2RP2002188	2888	2889
NT2RP2002232	C-NT2RP2002232	2890	2891
NT2RP2002304	C-NT2RP2002304	2892	2893
NT2RP2002409	C-NT2RP2002409	2894	2895
NT2RP2002510	C-NT2RP2002510	2896	2897
NT2RP2002527	C-NT2RP2002527	2898	2899
NT2RP2002533	C-NT2RP2002533	2900	2901

NT2RP2002564	C-NT2RP2002564	2902	2903
NT2RP2002674	C-NT2RP2002674	2904	2905
NT2RP2002721	C-NT2RP2002721	2906	2907
NT2RP2002824	C-NT2RP2002824	2908	2909
NT2RP2002942	C-NT2RP2002942	2910	2911
NT2RP2002974	C-NT2RP2002974	2912	2913
NT2RP2002976	C-NT2RP2002976	2914	2915
NT2RP2003042	C-NT2RP2003042	2916	2917
NT2RP2003179	C-NT2RP2003179	2918	2919
NT2RP2003210	C-NT2RP2003210	2920	2921
NT2RP2003369	C-NT2RP2003369	2922	2923
NT2RP2003383	C-NT2RP2003383	2924	2925
NT2RP2003469	C-NT2RP2003469	2926	2927
NT2RP2003545	C-NT2RP2003545	2928	2929
NT2RP2003593	C-NT2RP2003593	2930	2931
NT2RP2003599	C-NT2RP2003599	2932	2933
NT2RP2003655	C-NT2RP2003655	2934	2935
NT2RP2003931	C-NT2RP2003931	2936	2937
NT2RP2004141	C-NT2RP2004141	2938	2939
NT2RP2004179	C-NT2RP2004179	2940	2941
NT2RP2004205	C-NT2RP2004205	2942	2943
NT2RP2004447	C-NT2RP2004447	2944	2945
NT2RP2004495	C-NT2RP2004495	2946	2947
NT2RP2004524	C-NT2RP2004524	2948	2949
NT2RP2004556	C-NT2RP2004556	2950	2951
NT2RP2004606	C-NT2RP2004606	2952	2953
NT2RP2004648	C-NT2RP2004648	2954	2955
NT2RP2004670	C-NT2RP2004670	2956	2957
NT2RP2004794	C-NT2RP2004794	2958	2959
NT2RP2004837	C-NT2RP2004837	2960	2961
NT2RP2004847	C-NT2RP2004847	2962	2963
nnnnnnnnnnnn	C-nnnnnnnnnnnn	nnnn	nnnn
NT2RP2005027	C-NT2RP2005027	2966	
NT2RP2005163	C-NT2RP2005163	2967	2968
NT2RP2005181	C-NT2RP2005181	2969	2970
NT2RP2005247	C-NT2RP2005247	2971	2972
NT2RP2005425	C-NT2RP2005425	2973	2974
NT2RP2005463	C-NT2RP2005463	2975	2976
NT2RP2005514	C-NT2RP2005514	2977	2978
NT2RP2005541	C-NT2RP2005541	2979	2980
NT2RP2005632	C-NT2RP2005632	2981	2982
NT2RP2005878	C-NT2RP2005878	2983	2984
NT2RP2005883	C-NT2RP2005883	2985	2986
NT2RP2005887	C-NT2RP2005887	2987	2988
NT2RP2005941	C-NT2RP2005941	2989	2990
NT2RP2005994	C-NT2RP2005994	2991	2992
NT2RP2006042	C-NT2RP2006042	2993	2994
NT2RP2006269	C-NT2RP2006269	2995	2996
NT2RP2006512	C-NT2RP2006512	2997	2998
NT2RP3000059	C-NT2RP3000059	2999	3000
NT2RP3000063	C-NT2RP3000063	3001	3002
NT2RP3000125	C-NT2RP3000125	3003	3004

NT2RP3000169	C-NT2RP3000169	3005	3006
NT2RP3000172	C-NT2RP3000172	3007	3008
NT2RP3000201	C-NT2RP3000201	3009	3010
NT2RP3000436	C-NT2RP3000436	3011	3012
NT2RP3000460	C-NT2RP3000460	3013	3014
NT2RP3000616	C-NT2RP3000616	3015	3016
NT2RP3000721	C-NT2RP3000721	3017	3018
NT2RP3000820	C-NT2RP3000820	3019	3020
NT2RP3000871	C-NT2RP3000871	3021	3022
NT2RP3000907	C-NT2RP3000907	3023	3024
NT2RP3001012	C-NT2RP3001012	3025	3026
NT2RP3001044	C-NT2RP3001044	3027	3028
NT2RP3001061	C-NT2RP3001061	3029	3030
NT2RP3001170	C-NT2RP3001170	3031	3032
NT2RP3001195	C-NT2RP3001195	3033	3034
NT2RP3001240	C-NT2RP3001240	3035	3036
NT2RP3001322	C-NT2RP3001322	3037	3038
NT2RP3001388	C-NT2RP3001388	3039	3040
nnnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn
nnnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn
NT2RP3001560	C-NT2RP3001560	3045	3046
NT2RP3001592	C-NT2RP3001592	3047	3048
NT2RP3001738	C-NT2RP3001738	3049	3050
NT2RP3001754	C-NT2RP3001754	3051	3052
NT2RP3001858	C-NT2RP3001858	3053	3054
NT2RP3002160	C-NT2RP3002160	3055	3056
NT2RP3002311	C-NT2RP3002311	3057	3058
NT2RP3002342	C-NT2RP3002342	3059	3060
NT2RP3002448	C-NT2RP3002448	3061	3062
NT2RP3002721	C-NT2RP3002721	3063	3064
NT2RP3002738	C-NT2RP3002738	3065	3066
NT2RP3002790	C-NT2RP3002790	3067	3068
NT2RP3002836	C-NT2RP3002836	3069	3070
NT2RP3002958	C-NT2RP3002958	3071	3072
NT2RP3003000	C-NT2RP3003000	3073	3074
NT2RP3003076	C-NT2RP3003076	3075	3076
NT2RP3003354	C-NT2RP3003354	3077	3078
NT2RP3003469	C-NT2RP3003469	3079	3080
NT2RP3003527	C-NT2RP3003527	3081	3082
NT2RP3003535	C-NT2RP3003535	3083	3084
NT2RP3003559	C-NT2RP3003559	3085	3086
NT2RP3003614	C-NT2RP3003614	3087	3088
NT2RP3003729	C-NT2RP3003729	3089	3090
NT2RP3003849	C-NT2RP3003849	3091	3092
NT2RP3003874	C-NT2RP3003874	3093	3094
NT2RP3003963	C-NT2RP3003963	3095	3096
NT2RP3004000	C-NT2RP3004000	3097	3098
NT2RP3004075	C-NT2RP3004075	3099	3100
NT2RP3004083	C-NT2RP3004083	3101	3102
NT2RP3004090	C-NT2RP3004090	3103	3104
NT2RP3004130	C-NT2RP3004130	3105	3106
NT2RP3004133	C-NT2RP3004133	3107	3108

NT2RP3004202	C-NT2RP3004202	3109	3110
NT2RP3004309	C-NT2RP3004309	3111	3112
NT2RP3004321	C-NT2RP3004321	3113	3114
NT2RP3004355	C-NT2RP3004355	3115	3116
NT2RP3004374	C-NT2RP3004374	3117	3118
NT2RP3004406	C-NT2RP3004406	3119	3120
NT2RP3004552	C-NT2RP3004552	3121	3122
NT2RP3004557	C-NT2RP3004557	3123	3124
NT2RP3004625	C-NT2RP3004625	3125	3126
NT2RP3004640	C-NT2RP3004640	3127	3128
NT2RP3004647	C-NT2RP3004647	3129	3130
NT2RP4000108	C-NT2RP4000108	3131	3132
NT2RP4000962	C-NT2RP4000962	3133	3134
NT2RP4001009	C-NT2RP4001009	3135	3136
NT2RP4001467	C-NT2RP4001467	3137	3138
OVARC1000090	C-OVARC1000090	3139	
OVARC1000105	C-OVARC1000105	3140	3141
OVARC1000137	C-OVARC1000137	3142	
OVARC1000208	C-OVARC1000208	3143	
OVARC1000255	C-OVARC1000255	3144	3145
OVARC1000275	C-OVARC1000275	3146	3147
OVARC1000298	C-OVARC1000298	3148	3149
OVARC1000410	C-OVARC1000410	3150	3151
OVARC1000439	C-OVARC1000439	3152	3153
OVARC1000467	C-OVARC1000467	3154	3155
OVARC1000529	C-OVARC1000529	3156	3157
OVARC1000775	C-OVARC1000775	3158	3159
[illegible]	C-[illegible]	[illegible]	[illegible]
OVARC1000811	C-OVARC1000811	3162	3163
OVARC1000853	C-OVARC1000853	3164	3165
OVARC1000916	C-OVARC1000916	3166	3167
OVARC1000956	C-OVARC1000956	3168	3169
OVARC1001030	C-OVARC1001030	3170	3171
OVARC1001049	C-OVARC1001049	3172	3173
OVARC1001086	C-OVARC1001086	3174	3175
OVARC1001132	C-OVARC1001132	3176	3177
OVARC1001163	C-OVARC1001163	3178	3179
OVARC1001222	C-OVARC1001222	3180	
OVARC1001338	C-OVARC1001338	3181	3182
OVARC1001569	C-OVARC1001569	3183	3184
OVARC1001596	C-OVARC1001596	3185	3186
OVARC1001725	C-OVARC1001725	3187	
OVARC1001727	C-OVARC1001727	3188	
OVARC1001807	C-OVARC1001807	3189	3190
OVARC1001991	C-OVARC1001991	3191	3192
OVARC1002058	C-OVARC1002058	3193	3194
OVARC1002178	C-OVARC1002178	3195	
PLACE1000033	C-PLACE1000033	3196	3197
PLACE1000231	C-PLACE1000231	3198	3199
PLACE1000258	C-PLACE1000258	3200	3201
PLACE1000442	C-PLACE1000442	3202	3203
PLACE1000560	C-PLACE1000560	3204	3205

PLACE1000740	C-PLACE1000740	3206	3207
PLACE1000912	C-PLACE1000912	3208	3209
PLACE1000914	C-PLACE1000914	3210	3211
PLACE1000927	C-PLACE1000927	3212	3213
PLACE1001016	C-PLACE1001016	3214	3215
nnnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn
PLACE1001100	C-PLACE1001100	3218	
PLACE1001114	C-PLACE1001114	3219	3220
PLACE1001123	C-PLACE1001123	3221	
PLACE1001183	C-PLACE1001183	3222	3223
PLACE1001229	C-PLACE1001229	3224	3225
PLACE1001231	C-PLACE1001231	3226	3227
nnnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn
PLACE1001340	C-PLACE1001340	3230	3231
PLACE1001401	C-PLACE1001401	3232	3233
PLACE1001407	C-PLACE1001407	3234	3235
PLACE1001464	C-PLACE1001464	3236	3237
PLACE1001500	C-PLACE1001500	3238	3239
PLACE1001516	C-PLACE1001516	3240	3241
PLACE1001536	C-PLACE1001536	3242	3243
PLACE1001564	C-PLACE1001564	3244	3245
PLACE1001655	C-PLACE1001655	3246	3247
nnnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn
PLACE1001788	C-PLACE1001788	3250	3251
PLACE1001795	C-PLACE1001795	3252	3253
PLACE1001836	C-PLACE1001836	3254	3255
PLACE1001918	C-PLACE1001918	3256	3257
PLACE1001949	C-PLACE1001949	3258	3259
PLACE1002080	C-PLACE1002080	3260	3261
PLACE1002095	C-PLACE1002095	3262	3263
PLACE1002153	C-PLACE1002153	3264	3265
PLACE1002329	C-PLACE1002329	3266	3267
PLACE1002355	C-PLACE1002355	3268	3269
PLACE1002374	C-PLACE1002374	3270	3271
PLACE1002518	C-PLACE1002518	3272	3273
PLACE1002547	C-PLACE1002547	3274	3275
PLACE1002726	C-PLACE1002726	3276	3277
PLACE1002905	C-PLACE1002905	3278	3279
PLACE1002911	C-PLACE1002911	3280	3281
PLACE1002967	C-PLACE1002967	3282	3283
PLACE1003135	C-PLACE1003135	3284	3285
PLACE1003163	C-PLACE1003163	3286	3287
PLACE1003428	C-PLACE1003428	3288	3289
PLACE1003438	C-PLACE1003438	3290	3291
PLACE1003460	C-PLACE1003460	3292	3293
PLACE1003529	C-PLACE1003529	3294	3295
PLACE1003573	C-PLACE1003573	3296	3297
PLACE1003598	C-PLACE1003598	3298	3299
PLACE1003644	C-PLACE1003644	3300	
PLACE1003737	C-PLACE1003737	3301	3302
PLACE1003772	C-PLACE1003772	3303	3304
PLACE1003839	C-PLACE1003839	3305	3306

PLACE1003845	C-PLACE1003845	3307	3308
PLACE1003852	C-PLACE1003852	3309	3310
PLACE1004028	C-PLACE1004028	3311	
PLACE1004166	C-PLACE1004166	3312	3313
PLACE1004168	C-PLACE1004168	3314	3315
PLACE1004199	C-PLACE1004199	3316	3317
PLACE1004279	C-PLACE1004279	3318	3319
PLACE1004282	C-PLACE1004282	3320	3321
PLACE1004305	C-PLACE1004305	3322	3323
PLACE1004441	C-PLACE1004441	3324	3325
PLACE1004450	C-PLACE1004450	3326	3327
PLACE1004482	C-PLACE1004482	3328	3329
PLACE1004519	C-PLACE1004519	3330	3331
PLACE1004520	C-PLACE1004520	3332	3333
PLACE1004630	C-PLACE1004630	3334	3335
PLACE1004637	C-PLACE1004637	3336	3337
PLACE1004648	C-PLACE1004648	3338	3339
[illegible]	C-[illegible]	[illegible]	[illegible]
PLACE1004816	C-PLACE1004816	3342	3343
PLACE1004887	C-PLACE1004887	3344	3345
PLACE1005003	C-PLACE1005003	3346	3347
PLACE1005005	C-PLACE1005005	3348	3349
PLACE1005031	C-PLACE1005031	3350	3351
PLACE1005239	C-PLACE1005239	3352	3353
PLACE1005250	C-PLACE1005250	3354	3355
PLACE1005383	C-PLACE1005383	3356	3357
PLACE1005410	C-PLACE1005410	3358	3359
PLACE1005426	C-PLACE1005426	3360	3361
PLACE1005519	C-PLACE1005519	3362	3363
PLACE1005544	C-PLACE1005544	3364	3365
PLACE1005660	C-PLACE1005660	3366	3367
PLACE1005669	C-PLACE1005669	3368	3369
PLACE1005682	C-PLACE1005682	3370	3371
PLACE1005725	C-PLACE1005725	3372	3373
PLACE1005736	C-PLACE1005736	3374	3375
PLACE1005768	C-PLACE1005768	3376	3377
PLACE1005878	C-PLACE1005878	3378	3379
PLACE1006093	C-PLACE1006093	3380	3381
PLACE1006208	C-PLACE1006208	3382	3383
PLACE1006219	C-PLACE1006219	3384	3385
PLACE1006277	C-PLACE1006277	3386	3387
PLACE1006290	C-PLACE1006290	3388	3389
PLACE1006443	C-PLACE1006443	3390	3391
PLACE1006515	C-PLACE1006515	3392	3393
PLACE1006716	C-PLACE1006716	3394	3395
PLACE1006809	C-PLACE1006809	3396	3397
PLACE1006959	C-PLACE1006959	3398	3399
PLACE1007028	C-PLACE1007028	3400	3401
PLACE1007040	C-PLACE1007040	3402	3403
PLACE1007096	C-PLACE1007096	3404	3405
[illegible]	C-[illegible]	[illegible]	[illegible]
PLACE1007296	C-PLACE1007296	3408	3409

PLACE1007591	C-PLACE1007591	3410	
PLACE1007626	C-PLACE1007626	3411	3412
PLACE1007702	C-PLACE1007702	3413	3414
PLACE1007845	C-PLACE1007845	3415	3416
PLACE1007881	C-PLACE1007881	3417	3418
PLACE1008297	C-PLACE1008297	3419	3420
PLACE1008469	C-PLACE1008469	3423	3424
PLACE1008549	C-PLACE1008549	3425	3426
PLACE1008657	C-PLACE1008657	3427	3428
PLACE1008716	C-PLACE1008716	3429	3430
PLACE1008984	C-PLACE1008984	3431	3432
PLACE1008985	C-PLACE1008985	3433	3434
PLACE1009067	C-PLACE1009067	3435	3436
PLACE1009196	C-PLACE1009196	3437	3438
PLACE1009279	C-PLACE1009279	3439	3440
PLACE1009527	C-PLACE1009527	3441	3442
PLACE1009546	C-PLACE1009546	3443	3444
PLACE1009600	C-PLACE1009600	3445	3446
PLACE1009735	C-PLACE1009735	3447	3448
PLACE1009982	C-PLACE1009982	3449	3450
PLACE1010078	C-PLACE1010078	3451	3452
PLACE1010081	C-PLACE1010081	3453	3454
PLACE1010251	C-PLACE1010251	3455	3456
PLACE1010784	C-PLACE1010784	3457	3458
PLACE1010827	C-PLACE1010827	3459	3460
PLACE1010968	C-PLACE1010968	3461	3462
PLACE1011045	C-PLACE1011045	3463	3464
PLACE1011116	C-PLACE1011116	3465	3466
PLACE1011236	C-PLACE1011236	3467	3468
PLACE1011407	C-PLACE1011407	3469	3470
PLACE1011516	C-PLACE1011516	3471	3472
PLACE1011708	C-PLACE1011708	3473	3474
PLACE1011824	C-PLACE1011824	3475	3476
PLACE1011978	C-PLACE1011978	3477	3478
PLACE2000118	C-PLACE2000118	3479	3480
PLACE2000219	C-PLACE2000219	3481	
SKNMC1000004	C-SKNMC1000004	3482	3483
THYRO1000036	C-THYRO1000036	3484	3485
THYRO1000061	C-THYRO1000061	3486	3487
THYRO1000099	C-THYRO1000099	3488	3489
THYRO1000196	C-THYRO1000196	3490	3491
THYRO1000400	C-THYRO1000400	3492	3493
THYRO1000580	C-THYRO1000580	3494	3495
THYRO1000584	C-THYRO1000584	3496	3497
THYRO1000678	C-THYRO1000678	3498	3499
THYRO1000795	C-THYRO1000795	3500	3501
THYRO1000846	C-THYRO1000846	3502	3503
THYRO1000866	C-THYRO1000866	3504	3505
THYRO1000956	C-THYRO1000956	3506	3507
THYRO1000999	C-THYRO1000999	3508	
THYRO1001063	C-THYRO1001063	3509	3510

THYRO1001071	C-THYRO1001071	3511	3512
THYRO1001102	C-THYRO1001102	3513	3514
THYRO1001113	C-THYRO1001113	3515	3516
THYRO1001128	C-THYRO1001128	3517	3518
THYRO1001205	C-THYRO1001205	3519	3520
THYRO1001237	C-THYRO1001237	3521	3522
THYRO1001266	C-THYRO1001266	3523	3524
THYRO1001327	C-THYRO1001327	3525	3526
THYRO1001456	C-THYRO1001456	3527	3528
THYRO1001457	C-THYRO1001457	3529	3530
THYRO1001471	C-THYRO1001471	3531	3532
THYRO1001478	C-THYRO1001478	3533	3534
THYRO1001495	C-THYRO1001495	3535	3536
THYRO1001523	C-THYRO1001523	3537	3538
THYRO1001529	C-THYRO1001529	3539	3540
THYRO1001700	C-THYRO1001700	3541	3542
THYRO1001702	C-THYRO1001702	3543	3544
THYRO1001725	C-THYRO1001725	3545	3546
THYRO1001803	C-THYRO1001803	3547	3548
Y79AA1000127	C-Y79AA1000127	3549	3550
Y79AA1000207	C-Y79AA1000207	3551	3552
Y79AA1000226	C-Y79AA1000226	3553	3554
Y79AA1000270	C-Y79AA1000270	3555	3556
Y79AA1000426	C-Y79AA1000426	3557	3558
Y79AA1000521	C-Y79AA1000521	3559	3560
Y79AA1000776	C-Y79AA1000776	3561	3562
Y79AA1000777	C-Y79AA1000777	3563	3564
[illegible]	C-[illegible]	[illegible]	[illegible]
Y79AA1000876	C-Y79AA1000876	3567	3568
Y79AA1000959	C-Y79AA1000959	3569	3570
Y79AA1000967	C-Y79AA1000967	3571	3572
Y79AA1001013	C-Y79AA1001013	3573	3574
Y79AA1001056	C-Y79AA1001056	3575	3576
Y79AA1001062	C-Y79AA1001062	3577	3578
Y79AA1001090	C-Y79AA1001090	3579	3580
Y79AA1001264	C-Y79AA1001264	3581	3582
Y79AA1001272	C-Y79AA1001272	3583	3584
Y79AA1001328	C-Y79AA1001328	3585	3586
Y79AA1001430	C-Y79AA1001430	3587	3588
Y79AA1002022	C-Y79AA1002022	3589	3590
BNGH41000020	C-BNGH41000020	3595	3596
BNGH41000091	C-BNGH41000091	3597	3598
HEMBA1000462	C-HEMBA1000462	3599	3600
HEMBA1000477	C-HEMBA1000477	3601	3602
HEMBA1000671	C-HEMBA1000671	3603	3604
HEMBA1000732	C-HEMBA1000732	3605	3606
HEMBA1000835	C-HEMBA1000835	3607	3608
HEMBA1000875	C-HEMBA1000875	3609	
HEMBA1001184	C-HEMBA1001184	3610	
HEMBA1001272	C-HEMBA1001272	3611	
HEMBA1001296	C-HEMBA1001296	3612	

HEMBA1002048	C-HEMBA1002048	3613	3614
HEMBA1002985	C-HEMBA1002985	3615	3616
HEMBA1003120	C-HEMBA1003120	3617	3618
HEMBA1003497	C-HEMBA1003497	3619	3620
HEMBA1004007	C-HEMBA1004007	3621	
HEMBA1004085	C-HEMBA1004085	3622	3623
HEMBA1004785	C-HEMBA1004785	3624	3625
HEMBA1004952	C-HEMBA1004952	3626	
HEMBA1004971	C-HEMBA1004971	3627	
HEMBA1005230	C-HEMBA1005230	3628	
HEMBA1005246	C-HEMBA1005246	3629	3630
HEMBA1005267	C-HEMBA1005267	3631	3632
HEMBA1006276	C-HEMBA1006276	3633	
HEMBA1006357	C-HEMBA1006357	3634	3635
HEMBA1006517	C-HEMBA1006517	3636	3637
HEMBA1006544	C-HEMBA1006544	3638	3639
HEMBA1006749	C-HEMBA1006749	3640	3641
HEMBA1006770	C-HEMBA1006770	3642	3643
HEMBA1006912	C-HEMBA1006912	3644	
HEMBA1007063	C-HEMBA1007063	3645	3646
HEMBB1000106	C-HEMBB1000106	3647	3648
HEMBB1000407	C-HEMBB1000407	3649	3650
HEMBB1000542	C-HEMBB1000542	3651	3652
HEMBB1001547	C-HEMBB1001547	3653	3654
HEMBB1001959	C-HEMBB1001959	3655	3656
HEMBB1002039	C-HEMBB1002039	3657	
HEMBB1002041	C-HEMBB1002041	3658	3659
HEMBB1002051	C-HEMBB1002051	3660	3661
HEMBB1002120	C-HEMBB1002120	3662	3663
HEMBB1002302	C-HEMBB1002302	3664	3665
HEMBB1002661	C-HEMBB1002661	3666	3667
MAMMA1000106	C-MAMMA1000106	3668	3669
MAMMA1000141	C-MAMMA1000141	3670	3671
MAMMA1000204	C-MAMMA1000204	3672	3673
MAMMA1000226	C-MAMMA1000226	3674	3675
MAMMA1000403	C-MAMMA1000403	3676	3677
MAMMA1000473	C-MAMMA1000473	3678	3679
MAMMA1000496	C-MAMMA1000496	3680	3681
MAMMA1000528	C-MAMMA1000528	3682	
MAMMA1000614	C-MAMMA1000614	3683	3684
MAMMA1000652	C-MAMMA1000652	3685	
MAMMA1000706	C-MAMMA1000706	3686	3687
MAMMA1000788	C-MAMMA1000788	3688	3689
MAMMA1000810	C-MAMMA1000810	3690	3691
MAMMA1000814	C-MAMMA1000814	3692	3693
MAMMA1000881	C-MAMMA1000881	3694	3695
MAMMA1000986	C-MAMMA1000986	3696	3697
MAMMA1000994	C-MAMMA1000994	3698	3699
MAMMA1001141	C-MAMMA1001141	3700	3701
MAMMA1001150	C-MAMMA1001150	3702	3703
MAMMA1001237	C-MAMMA1001237	3704	3705
MAMMA1001284	C-MAMMA1001284	3706	3707

MAMMA1001310	C-MAMMA1001310	3708	3709
MAMMA1001344	C-MAMMA1001344	3710	3711
MAMMA1001418	C-MAMMA1001418	3712	3713
MAMMA1001532	C-MAMMA1001532	3714	3715
MAMMA1001615	C-MAMMA1001615	3716	3717
MAMMA1001623	C-MAMMA1001623	3718	3719
MAMMA1001634	C-MAMMA1001634	3720	3721
MAMMA1001957	C-MAMMA1001957	3722	3723
MAMMA1001978	C-MAMMA1001978	3724	3725
MAMMA1002070	C-MAMMA1002070	3726	3727
MAMMA1002080	C-MAMMA1002080	3728	3729
MAMMA1002087	C-MAMMA1002087	3730	3731
MAMMA1002095	C-MAMMA1002095	3732	3733
MAMMA1002128	C-MAMMA1002128	3734	3735
MAMMA1002142	C-MAMMA1002142	3736	3737
MAMMA1002165	C-MAMMA1002165	3738	3739
MAMMA1002205	C-MAMMA1002205	3740	
MAMMA1002234	C-MAMMA1002234	3741	3742
MAMMA1002586	C-MAMMA1002586	3743	3744
MAMMA1002633	C-MAMMA1002633	3745	3746
MAMMA1003126	C-MAMMA1003126	3747	3748
NT2RM1000580	C-NT2RM1000580	3749	3750
NT2RM1000858	C-NT2RM1000858	3751	3752
NT2RM2000565	C-NT2RM2000565	3753	3754
NT2RM2000582	C-NT2RM2000582	3755	
NT2RM2000589	C-NT2RM2000589	3756	3757
NT2RM2000632	C-NT2RM2000632	3758	3759
NT2RM2000773	C-NT2RM2000773	3760	
NT2RM2001558	C-NT2RM2001558	3761	3762
NT2RM2001626	C-NT2RM2001626	3763	3764
NT2RM2001643	C-NT2RM2001643	3765	3766
NT2RM2001738	C-NT2RM2001738	3767	3768
NT2RM2001792	C-NT2RM2001792	3769	3770
NT2RM2001818	C-NT2RM2001818	3771	3772
NT2RM4000100	C-NT2RM4000100	3773	3774
NT2RM4000115	C-NT2RM4000115	3775	3776
NT2RM4000417	C-NT2RM4000417	3777	3778
NT2RM4000593	C-NT2RM4000593	3779	3780
NT2RM4000761	C-NT2RM4000761	3781	3782
NT2RM4000965	C-NT2RM4000965	3783	3784
NT2RM4001377	C-NT2RM4001377	3785	3786
NT2RM4001768	C-NT2RM4001768	3787	3788
NT2RM4001843	C-NT2RM4001843	3789	3790
NT2RP1000239	C-NT2RP1000239	3791	3792
NT2RP1000465	C-NT2RP1000465	3793	3794
NT2RP1000468	C-NT2RP1000468	3795	3796
NT2RP1000679	C-NT2RP1000679	3797	3798
NT2RP1000740	C-NT2RP1000740	3799	3800
NT2RP1001031	C-NT2RP1001031	3801	3802
NT2RP2000178	C-NT2RP2000178	3803	3804
NT2RP2000240	C-NT2RP2000240	3805	
NT2RP2000447	C-NT2RP2000447	3806	3807

NT2RP2000610	C-NT2RP2000610	3808	3809
NT2RP2000616	C-NT2RP2000616	3810	3811
NT2RP2000712	C-NT2RP2000712	3812	3813
NT2RP2000739	C-NT2RP2000739	3814	3815
NT2RP2000818	C-NT2RP2000818	3816	3817
NT2RP2001200	C-NT2RP2001200	3818	3819
NT2RP2001223	C-NT2RP2001223	3820	3821
NT2RP2001276	C-NT2RP2001276	3822	3823
NT2RP2001388	C-NT2RP2001388	3824	3825
NT2RP2001469	C-NT2RP2001469	3826	3827
NT2RP2001562	C-NT2RP2001562	3828	3829
NT2RP2001662	C-NT2RP2001662	3830	3831
NT2RP2001755	C-NT2RP2001755	3832	3833
NT2RP2001817	C-NT2RP2001817	3834	3835
NT2RP2001948	C-NT2RP2001948	3836	3837
NT2RP2002015	C-NT2RP2002015	3838	3839
NT2RP2003390	C-NT2RP2003390	3840	3841
NT2RP2003664	C-NT2RP2003664	3842	3843
NT2RP2003940	C-NT2RP2003940	3844	3845
NT2RP2004069	C-NT2RP2004069	3846	3847
NT2RP2004108	C-NT2RP2004108	3848	3849
nnnnnnnnnnnn	C-nnnnnnnnnnnn	3850	3851
NT2RP2005069	C-NT2RP2005069	3852	3853
NT2RP2005378	C-NT2RP2005378	3854	3855
NT2RP2005391	C-NT2RP2005391	3856	3857
NT2RP2005597	C-NT2RP2005597	3858	3859
NT2RP2005666	C-NT2RP2005666	3860	3861
NT2RP2006004	C-NT2RP2006004	3862	3863
NT2RP2006092	C-NT2RP2006092	3864	3865
NT2RP2006134	C-NT2RP2006134	3866	3867
NT2RP3000011	C-NT2RP3000011	3868	3869
NT2RP3000022	C-NT2RP3000022	3870	3871
NT2RP3000171	C-NT2RP3000171	3872	3873
NT2RP3000304	C-NT2RP3000304	3874	3875
NT2RP3000378	C-NT2RP3000378	3876	3877
NT2RP3000444	C-NT2RP3000444	3878	3879
NT2RP3000645	C-NT2RP3000645	3880	3881
NT2RP3000676	C-NT2RP3000676	3882	3883
NT2RP3000677	C-NT2RP3000677	3884	3885
NT2RP3000789	C-NT2RP3000789	3886	3887
NT2RP3000818	C-NT2RP3000818	3888	3889
NT2RP3000838	C-NT2RP3000838	3890	3891
NT2RP3000921	C-NT2RP3000921	3892	3893
NT2RP3001159	C-NT2RP3001159	3894	3895
NT2RP3001271	C-NT2RP3001271	3896	3897
NT2RP3001542	C-NT2RP3001542	3898	3899
NT2RP3001685	C-NT2RP3001685	3900	3901
NT2RP3001976	C-NT2RP3001976	3902	3903
NT2RP3002015	C-NT2RP3002015	3904	3905
NT2RP3002281	C-NT2RP3002281	3906	3907
NT2RP3002286	C-NT2RP3002286	3908	3909
NT2RP3002324	C-NT2RP3002324	3910	3911

NT2RP3002353	C-NT2RP3002353	3912	3913
NT2RP3002571	C-NT2RP3002571	3914	3915
NT2RP3002664	C-NT2RP3002664	3916	3917
NT2RP3002737	C-NT2RP3002737	3918	3919
NT2RP3002887	C-NT2RP3002887	3920	3921
NT2RP3002900	C-NT2RP3002900	3922	3923
NT2RP3002983	C-NT2RP3002983	3924	3925
NT2RP3003473	C-NT2RP3003473	3926	3927
NT2RP3003532	C-NT2RP3003532	3928	3929
NT2RP3004025	C-NT2RP3004025	3930	3931
NT2RP3004067	C-NT2RP3004067	3932	3933
NT2RP3004119	C-NT2RP3004119	3934	3935
NT2RP3004294	C-NT2RP3004294	3936	3937
NT2RP3004345	C-NT2RP3004345	3938	3939
NT2RP4000634	C-NT2RP4000634	3940	3941
NT2RP4001001	C-NT2RP4001001	3942	3943
NT2RP4001877	C-NT2RP4001877	3944	3945
NT2RP4001879	C-NT2RP4001879	3946	3947
NT2RP4002187	C-NT2RP4002187	3948	3949
NT2RP4002451	C-NT2RP4002451	3950	3951
NT2RP4002750	C-NT2RP4002750	3952	3953
OVARC1000003	C-OVARC1000003	3954	3955
OVARC1000313	C-OVARC1000313	3956	3957
OVARC1000331	C-OVARC1000331	3958	3959
OVARC1000553	C-OVARC1000553	3960	3961
OVARC1000873	C-OVARC1000873	3962	3963
OVARC1000995	C-OVARC1000995	3964	
OVARC1001260	C-OVARC1001260	3965	
OVARC1001336	C-OVARC1001336	3966	3967
OVARC1001570	C-OVARC1001570	3968	3969
OVARC1001607	C-OVARC1001607	3970	3971
OVARC1001833	C-OVARC1001833	3972	3973
OVARC1001952	C-OVARC1001952	3974	3975
PLACE1000986	C-PLACE1000986	3976	
PLACE1003407	C-PLACE1003407	3977	3978
PLACE1004078	C-PLACE1004078	3979	3980
PLACE1004492	C-PLACE1004492	3981	3982
PLACE1005539	C-PLACE1005539	3983	3984
PLACE1005569	C-PLACE1005569	3985	3986
PLACE1005601	C-PLACE1005601	3987	
PLACE1005745	C-PLACE1005745	3988	3989
PLACE1005815	C-PLACE1005815	3990	3991
PLACE1005927	C-PLACE1005927	3992	3993
PLACE1006071	C-PLACE1006071	3994	3995
PLACE1006073	C-PLACE1006073	3996	3997
PLACE1006079	C-PLACE1006079	3998	3999
PLACE1006786	C-PLACE1006786	4000	
PLACE1007077	C-PLACE1007077	4001	4002
PLACE1007971	C-PLACE1007971	4003	
PLACE1008282	C-PLACE1008282	4004	4005
PLACE1008359	C-PLACE1008359	4006	4007
PLACE1008744	C-PLACE1008744	4008	4009

PLACE1010445	C-PLACE1010445	4010	4011
PLACE1010713	C-PLACE1010713	4012	4013
nnnnnnnnnnnn	C-nnnnnnnnnnnn	4014	4015
PLACE1011181	C-PLACE1011181	4016	4017
PLACE1011364	C-PLACE1011364	4018	4019
PLACE3000181	C-PLACE3000181	4020	4021
SKNMC1000014	C-SKNMC1000014	4022	4023
SKNMC1000082	C-SKNMC1000082	4024	4025
THYRO1000964	C-THYRO1000964	4026	4027
THYRO1001242	C-THYRO1001242	4028	4029
THYRO1001608	C-THYRO1001608	4030	4031
THYRO1001641	C-THYRO1001641	4032	4033
THYRO1001770	C-THYRO1001770	4034	4035
Y79AA1000030	C-Y79AA1000030	4036	4037
Y79AA1001212	C-Y79AA1001212	4038	4039
Y79AA1001426	C-Y79AA1001426	4040	4041
Y79AA1001427	C-Y79AA1001427	4042	4043
Y79AA1001523	C-Y79AA1001523	4044	4045
Y79AA1001530	C-Y79AA1001530	4046	4047
Y79AA1001592	C-Y79AA1001592	4048	4049
Y79AA1001727	C-Y79AA1001727	4050	4051
Y79AA1001787	C-Y79AA1001787	4052	4053
Y79AA1001793	C-Y79AA1001793	4054	4055
Y79AA1001795	C-Y79AA1001795	4056	4057
Y79AA1001799	C-Y79AA1001799	4058	4059
Y79AA1001803	C-Y79AA1001803	4060	4061
Y79AA1001863	C-Y79AA1001863	4062	4063
Y79AA1002058	C-Y79AA1002058	4064	4065
Y79AA1002121	C-Y79AA1002121	4066	4067
Y79AA1002213	C-Y79AA1002213	4068	4069
Y79AA1002373	C-Y79AA1002373	4070	4071
Y79AA1002376	C-Y79AA1002376	4072	4073
Y79AA1002378	C-Y79AA1002378	4074	4075
Y79AA1002381	C-Y79AA1002381	4076	4077
BNGH41000087	C-BNGH41000087	4078	4079
HEMBA1001886	C-HEMBA1001886	4080	4081
HEMBA1004067	C-HEMBA1004067	4082	4083
HEMBA1007226	C-HEMBA1007226	4084	4085
HEMBB1000309	C-HEMBB1000309	4086	4087
HEMBB1000567	C-HEMBB1000567	4088	4089
MAMMA1000102	C-MAMMA1000102	4090	4091
MAMMA1001066	C-MAMMA1001066	4092	4093
MAMMA1001094	C-MAMMA1001094	4094	4095
MAMMA1001609	C-MAMMA1001609	4096	4097
MAMMA1001901	C-MAMMA1001901	4098	
MAMMA1002091	C-MAMMA1002091	4099	4100
NT2RM1000462	C-NT2RM1000462	4101	4102
NT2RM1000542	C-NT2RM1000542	4103	4104
NT2RM1000789	C-NT2RM1000789	4105	4106
NT2RM1000855	C-NT2RM1000855	4107	4108
NT2RM1000899	C-NT2RM1000899	4109	4110

NT2RP2000092	C-NT2RP2000092	4111	4112
NT2RP2001538	C-NT2RP2001538	4113	4114
NT2RP2001921	C-NT2RP2001921	4115	4116
NT2RP2003138	C-NT2RP2003138	4117	4118
NT2RP2003302	C-NT2RP2003302	4119	4120
NT2RP2003950	C-NT2RP2003950	4121	4122
NT2RP2005535	C-NT2RP2005535	4123	4124
NT2RP2005774	C-NT2RP2005774	4125	4126
NT2RP3000148	C-NT2RP3000148	4127	4128
NT2RP3000232	C-NT2RP3000232	4129	4130
NT2RP3000427	C-NT2RP3000427	4131	
NT2RP3000652	C-NT2RP3000652	4132	4133
NT2RP3001650	C-NT2RP3001650	4134	4135
NT2RP3002409	C-NT2RP3002409	4136	
NT2RP3002411	C-NT2RP3002411	4137	4138
NT2RP3003448	C-NT2RP3003448	4139	
NT2RP4002715	C-NT2RP4002715	4140	4141
OVARC1000307	C-OVARC1000307	4142	4143
PLACE1000907	C-PLACE1000907	4144	4145
PLACE1007081	C-PLACE1007081	4146	4147
PLACE1010011	C-PLACE1010011	4148	4149
PLACE3000213	C-PLACE3000213	4150	4151
PLACE4000354	C-PLACE4000354	4152	4153
PLACE4000455	C-PLACE4000455	4154	
THYRO1000776	C-THYRO1000776	4155	4156
THYRO1001593	C-THYRO1001593	4157	4158
Y79AA1000750	C-Y79AA1000750	4159	4160
Y79AA1000888	C-Y79AA1000888	4161	4162
Y79AA1002129	C-Y79AA1002129	4163	4164
Y79AA1002334	C-Y79AA1002334	4165	4166
MAMMA1002224	C-MAMMA1002224	4167	
NT2RP1000271	C-NT2RP1000271	4168	4169
NT2RP3000481	C-NT2RP3000481	4170	4171
NT2RP3004481	C-NT2RP3004481	4172	4173
HEMBA1006658	C-HEMBA1006658	4174	4175
NT2RP2006099	C-NT2RP2006099	4176	4177
NT2RP2006580	C-NT2RP2006580	4178	4179

Homology search result 1

[0287] The result of the homology search in the SwissProt using the representative sequences of the 5'-ends.

Indicated are from the top,
the name of the representative sequence of the cluster,
definition of the top hit data,
the P-value the length of the sequence used for comparison (nucleotide) similarity (%),
the organism of which the top hit data is obtained,
the Accession No. of the top hit data.

[0288] Homology search results of the representative sequences of the 5'-end cluster to the data in SwissProt database are shown only for the representative sequences of the cluster from which clones were selected based on the homology search results.

[0289] The P-value is the score which is determined by taking into account the statistic probability of occurrence between the two sequences, and generally low score reflects high similarity. (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

HRIFA000016a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
9.2e-05:178:32
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
P10496

HRIFA000071a
CIRCUMSPOROZOITE PROTEB PRECURSOR (CS).
5.8e-05:194:29
PLASMODIUM SIMIUM.
Q03110

HRIFA000116a
HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.
6.2e-06:83:27
CAENORHABDITIS ELEGANS.
P34679

HRIFA000123a
PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).
6.2e-08:89:34
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P33154

HRIFA000264a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
1.4e-06:231:34
GALLUS GALLUS (CHICKEN).
P02457

HRIFA000327a
ATP-BINDING CASSETTE TRANSPORTER 1.
2.0e-16:238:31
MUS MUSCULUS (MOUSE).
P41233

HRIFA000415a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.6e-06:120:35
MUS MUSCULUS (MOUSE).
P05142

HRIFA000432a
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.
2.2e-21:86:52
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09818

HRIFA000446a
HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.

2.5e-09:138:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40085

HRIFA000553a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
1.7e-27:117:48
GALLUS GALLUS (CHICKEN).
P05099

HRIFA000564a
ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).
2.9e-28:163:38
MUS MUSCULUS (MOUSE).
P54116

HRIFA000631a
ZINC FINGER PROTEIN 140.
8.2e-45:155:47
HOMO SAPIENS (HUMAN).
P52738

HRIFA000683a
FIBRILLIN 1 PRECURSOR.
4.8e-18:77:46
HOMO SAPIENS (HUMAN).
P35555

HRIFA000695a
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6 PEPTIDE P-H]
4.0e-06:105:33
HOMO SAPIENS (HUMAN).
P04280

HRIFA000776a
FIBRILLIN 2 PRECURSOR.
1.6e-42:214:44
HOMO SAPIENS (HUMAN).
P35556

HRIFA000814a
ZINC FINGER PROTEIN 133.
4.4e-16:49:87
HOMO SAPIENS (HUMAN).
P52736

HRIFA000845a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
6.0e-06:172:34
MUS MUSCULUS (MOUSE).
P11087

HRIFA001099a
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-5 (FRAGMENT).
0.92:38:34
HOMO SAPIENS (HUMAN).
P18849

HRIFA001132a
AGRIN PRECURSOR.
1.3e-26:239:32
GALLUS GALLUS (CHICKEN).
P31696

HRIFA001138a
CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP).
5.9e-114:147:83
HOMO SAPIENS (HUMAN).
P49747

HRIFA001200a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.035:119:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128

HRIFA001337a
LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR).
2.4e-17:98:42
CRICETULUS GRISEUS (CHINESE HAMSTER).
P35950

HRIFA001341a
NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L) (NF68).
1.2e-102:248:87
RATTUS NORVEGICUS (RAT).
P19527

HRIFA001413a
BACTENECIN 7 PRECURSOR (BAC7) (PR-59).
0.0032:33:63
BOS TAURUS (BOVINE).
P19661

HRIFA001439a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
0.00031:34:61
HOMO SAPIENS (HUMAN).
P20931

HRIFA001489a
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
8.4e-65:105:72
HOMO SAPIENS (HUMAN).
P35414

HRIFA001558a
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
0.0048:80:31
PLASMODIUM LOPHURAE.
P04929

HRIFA001712a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
2.5e-19:169:31

THERMOMONOSPORA CURVATA.
P49695

HRIFA001720a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.4e-94:273:64
HOMO SAPIENS (HUMAN).
Q03923

HRIFA001866a
EARLY ANTIGEN PROTEIN D (EA-D).
0.10:93:34
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03191

HRIFA001942a
"PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1)."
4.7e-12:140:30
GALLUS GALLUS (CHICKEN).
P24802

HRIFA001971a
HYPOTHETICAL 46.3 KD PROTEIN IN PTA1-CDC24 INTERGENIC REGION.
2.5e-10:86:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39727

HRIFA001972a
LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).
0.10:100:34
MUS MUSCULUS (MOUSE).
P19137

HRIFA001975a
ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
6.5e-30:243:33
MUS MUSCULUS (MOUSE).
P21836

HRIFA001984a
"PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1)."
1.2e-11:140:30
GALLUS GALLUS (CHICKEN).
P24802

HRIFA002063a
GNS1 PROTEIN.
1.3e-05:127:30
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).
P25358

HRIFA002102a
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
2.9e-07:241:30
HOMO SAPIENS (HUMAN).
Q02817

HRIFA002284a
ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).
3.8e-05:104:34
RATTUS NORVEGICUS (RAT).
P04474

HRIFA002309a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
1.5e-08:110:37
THERMOMONOSPORA CURVATA.
P49695

HRIFA002384a
GAP JUNCTION ALPHA-6 PROTEIN (CONNEXIN 45) (CX45).
1.8e-31:94:42
HOMO SAPIENS (HUMAN).
P36383

HRIFA002503a
N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).
6.1e-92:246:67
MUS MUSCULUS (MOUSE).
P15535

HRIFA002689a
TRANSCRIPTION FACTOR GATA-6 (GATA BINDING FACTOR-6) (DNA BINDING PROTEIN GATA-GT2).
0.38:49:34
RATTUS NORVEGICUS (RAT).
P46153

HRIFA002694a
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
4.7e-05:93:37
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602

HRIFA002743a
BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).
1.2e-23:216:31
HOMO SAPIENS (HUMAN).
P13497

HRIFA002762a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.1e-09:129:41
MUS MUSCULUS (MOUSE).
P05142

HRIFA002766a
FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).
1.8e-12:139:34
HOMO SAPIENS (HUMAN).
Q06828

HRIFA002787a
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.

1.6e-10:124:37
HOMO SAPIENS (HUMAN).
P08123

HRIFA002805a
ZINC FINGER PROTEIN 140.
3.6e-23:43:74
HOMO SAPIENS (HUMAN).
P52738

HRIFA002891a
"FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)."
2.0e-41:239:39
MUS MUSCULUS (MOUSE).
Q08878

HRIFA002919a
BEM46 PROTEIN (FRAGMENT).
1.0e-12:171:32
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P54069

HRIFA002980a
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR).
8.7e-32:202:37
GALLUS GALLUS (CHICKEN).
P98157

HRIFA003055a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.4e-08:175:29
MUS MUSCULUS (MOUSE).
P05142

HRIFA003063a
B-CELL LYMPHOMA 6 PROTEIN HOMOLOG.
2.8e-15:123:34
MUS MUSCULUS (MOUSE).
P41183

HRIFA003093a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.3e-11:142:37
MUS MUSCULUS (MOUSE).
P05142

HRIFA003340a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
2.3e-05:200:31
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

HRIFA003357a
GLUCOSE REPRESSION MEDIATOR PROTEIN.
0.0023:190:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14922

HRIFA003402a
COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).
3.6e-05:194:27
BOS TAURUS (BOVINE).
P02459

HRIFA003504a
CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).
1.4e-08:150:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
P33450

HRIFA003592a
CD9 ANTIGEN.
0.0053:24:70
BOS TAURUS (BOVINE).
P30932

HRIFA003635a
"MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE)."
5.3e-45:239:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P53624

HRIFA003640a
PROCYCLIC FORM SPECIFIC POLYPEPTIDE A-BETA PRECURSOR (PROCYCLIN) (PARP A-BETA).
0.00018:28:64
TRYPANOSOMA BRUCEI BRUCEI.
P09791

HRIFA003883a
TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (YIN AND YANG 1) (YY-1) (DELTA TRANSCRIPTION FACTOR) (NF-E1) (UCR-MOTIF DNA-BINDING PROTEIN).
1.0:57:35
MUS MUSCULUS (MOUSE).
Q00899

HRIFA003892a
MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).
6.5e-08:144:25
BACILLUS SUBTILIS.
P39843

HRIFA003946a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.4e-06:85:37
MUS MUSCULUS (MOUSE).
P05142

HRIFA004006a
ZINC FINGER PROTEIN 140.
6.2e-20:83:66
HOMO SAPIENS (HUMAN).
P52738

HRIFA004034a
B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).
1.4e-15:192:32
HOMO SAPIENS (HUMAN).
P20749

HRIFA004112a
CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).
7.2e-26:193:37
DROSOPHILA MELANOGASTER (FRUIT FLY).
P33450

HRIFA004162a
ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).
3.6e-10:117:29
MUS MUSCULUS (MOUSE).
P54116

HRIFA004401a
LACTOSE OPERON REPRESSOR.
1.1e-07:36:86
ESCHERICHIA COLI.
P03023

HRIFA004426a
ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).
5.1e-11:85:41
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
P15287

HRIFA004490a
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
5.3e-19:101:44
MUS MUSCULUS (MOUSE).
P23780

HRIFA004523a
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
2.6e-36:180:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

HRIFA004663a
T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7).
1.2e-40:112:75
MUS MUSCULUS (MOUSE).
Q00417

HRIFA004696a
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT
1.1e-62:145:84
CANIS FAMILIARIS (DOG).
P38377

HRIFA004714a
HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.
2.3e-50:127:54
CAENORHABDITIS ELEGANS.

Q09201

HRIFA004745a
MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
5.0e-17:107:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23500

HRIFA004780a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
7.2e-07:142:30
ZEA MAYS (MAIZE).
P14918

HRIFA004919a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
1.5e-25:156:46
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
P10496

HRIFA005072a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
8.3e-05:24:62
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157

HRIFA005102a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
2.5e-07:188:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

HRIFA005184a
CYTOCHROME B5.
3.4e-11:117:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40312

HRIFA005214a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
5.9e-05:141:33
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284

HRIFA005231a
ORM1 PROTEIN.
1.7e-18:137:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224

HRIFA005240a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
6.3e-81:194:70
HOMO SAPIENS (HUMAN).
Q03923

HRIFA005255a
HYPOTHETICAL 57.1 KD PROTEIN IN MAP2-TEL1 INTERGENIC REGION.

1.5e-07:202:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38176

HRIFA005271a
MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR.
1.2e-55:86:81
HOMO SAPIENS (HUMAN).
Q00325

HRIFA005296a
INSULIN PROMOTER FACTOR 1 (IPF-1) (ISLET/DUODENUM HOMEOBOX-1) (IDX-1) (SOMATOSTATIN TRANSACTIVATING FACTOR-1) (STF-1) (PANCREAS/DUODENUM HOMEOBOX-1) (GLUCOSE SENSITIVE FACTOR) (GSF).
0.82:90:34
HOMO SAPIENS (HUMAN).
P52945

HRIFA005300a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.6e-07:178:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA005369a
EBNA-1 NUCLEAR PROTEIN.
2.3e-07:101:39
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA005372a
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).
1.1e-14:97:38
PETROMYZON MARINUS (SEA LAMPREY).
P25210

HRIFA005392a
SYNDECAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2).
1.3e-50:126:84
HOMO SAPIENS (HUMAN).
P34741

HRIFA005409a
HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).
7.1e-66:197:64
HOMO SAPIENS (HUMAN).
P30825

HRIFA005420a
INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7) (TIS7 PROTEIN).
1.5e-33:221:41
MUS MUSCULUS (MOUSE).
P19182

HRIFA005438a
SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR (EC 1.3.5.1) (FP) (FLAVOPROTEIN SUBUNIT OF COMPLEX II).
6.4e-71:175:68
HOMO SAPIENS (HUMAN).
P31040

HRIFA005462a
CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).
1.4e-19:137:37
OVIS ARIES (SHEEP).
P08060

HRIFA005500a
EBNA-1 NUCLEAR PROTEIN.
0.00042:54:50
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA005540a
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).
0.12:47:29
HOMO SAPIENS (HUMAN).
P18850

HRIFA005644a
VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT)
1.2e-102:233:87
BOS TAURUS (BOVINE).
P40682

HRIFA005702a
CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELANOMA-ASSOCIATED ANTIGEN MUC18) (MELANOMA-ASSOCIATED ANTIGEN A32) (S-ENDO 1 ENDOTHELIAL- ASSOCIATED ANTIGEN) (CD146 ANTIGEN) (MELANOMA ADHESION MOLECULE).
8.7e-05:174:28
HOMO SAPIENS (HUMAN).
P43121

HRIFA005720a
F-SPONDIN PRECURSOR.
8.9e-12:155:31
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P35447

HRIFA005728a
SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).
1.7e-05:126:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08458

HRIFA005732a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
4.4e-26:159:38
THERMOMONOSPORA CURVATA.
P49695

HRIFA005760a

FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT).
3.8e-15:53:54
HOMO SAPIENS (HUMAN).
P16442

HRIFA005781a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).
5.2e-47:228:47
HOMO SAPIENS (HUMAN).
P37058

HRIFA005944a
PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].
2.5e-06:142:35
MUS MUSCULUS (MOUSE).
P28481

HRIFA006183a
ZINC FINGER PROTEIN 136.
1.3e-42:129:62
HOMO SAPIENS (HUMAN).
P52737

HRIFA006250a
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).
0.0038:75:37
DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439

HRIFA006298a
EBNA-1 NUCLEAR PROTEIN.
1.4e-05:80:42
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA006448a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
8.5e-05:183:28
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA006494a
AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).
1.2e-18:201:33
HOMO SAPIENS (HUMAN).
Q02246

HRIFA006510a
CORNICHON PROTEIN.
6.0e-53:144:66
DROSOPHILA MELANOGASTER (FRUIT FLY).
P49858

HRIFA006566a
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-

BOX DNA BINDING PROTEIN SUBUNIT B).
6.6e-15:97:38
PETROMYZON MARINUS (SEA LAMPREY).
P25210

HRIFA006572a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
7.2e-05:158:29
MUS MUSCULUS (MOUSE).
P11087

HRIFA006586a
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
1.3e-13:219:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981

HRIFA006596a
POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1) (PPSEP 1).
7.2e-22:241:32
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10071

HRIFA006609a
PANCREATIC HORMONE PRECURSOR (PANCREATIC POLYPEPTIDE) (PP).
0.61:28:46
"GALLUS GALLUS (CHICKEN), AND MELEAGRIS GALLOPAVO (COMMON TURKEY)."
P01306

HRIFA006633a
COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.
7.8e-07:170:34
HOMO SAPIENS (HUMAN).
Q07092

HRIFA006642a
AMALGAM PROTEIN PRECURSOR.
1.5e-09:185:28
DROSOPHILA MELANOGASTER (FRUIT FLY).
P15364

HRIFA006649a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.7e-50:166:50
HOMO SAPIENS (HUMAN).
Q03923

HRIFA006667a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
6 8e-45.180:43
HOMO SAPIENS (HUMAN).
Q03923

HRIFA006730a
SYG1 PROTEIN.
1.8e-14:164:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40528

HRIFA006798a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.22:149:34
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA006926a
SYNAPTOTAGMIN IV.
3.6e-19:168:38
RATTUS NORVEGICUS (RAT).
P50232

HRIFA007013a
MIC1 PROTEIN.
1.4e-13:115:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53258

HRIFA007032a
CCAAT DISPLACEMENT PROTEIN (HOMEOBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).
0.00013:92:35
CANIS FAMILIARIS (DOG).
P39881

HRIFA007068a
EBNA-1 NUCLEAR PROTEIN.
7.0e-10:145:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA007152a
TRANSCRIPTION FACTOR SOX-4.
0.90:47:44
HOMO SAPIENS (HUMAN).
Q06945

HRIFA007219a
THROMBOSPONDIN 3 PRECURSOR.
1.3e-105:209:88
HOMO SAPIENS (HUMAN).
P49746

HRIFA007228a
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
2.3e-11:174:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981

HRIFA007243a
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
3.0e-18:163:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986

HRIFA007244a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

4.2e-05:81:33
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

HRIFA007256a
DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
2.3e-77:186:75
HOMO SAPIENS (HUMAN).
P53355

HRIFA007262a
PAIRED AMPHIPATHIC HELIX PROTEIN.
1.3e-06:152:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579

HRIFA007352a
5'-TG-3'INTERACTING FACTOR (HOMEOBOX PROTEIN TGIF).
4.2e-36:146:57
HOMO SAPIENS (HUMAN).
Q15583

HRIFA007424a
F-SPONDIN PRECURSOR.
8.9e-34:84:89
RATTUS NORVEGICUS (RAT).
P35446

HRIFA007435a
PROTEIN KINASE CEK1 (EC 2.7.1.-).
1.0e-37:159:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P38938

HRIFA007463a
HST1 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 1).
4.8e-32:85:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53685

HRIFA007493a
UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).
1.2e-47:171:56
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P33296

HRIFA007512a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
8.0e-07:173:28
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

HRIFA007532a
"CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE SUBUNIT)."
1.8e-10:110:37

HOMO SAPIENS (HUMAN).
P20807

HRIFA007547a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.068:51:45
BOVINE HERPESVIRUS TYPE 1 (STRAIN K22).
P29836

HRIFA007565a
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
5.1e-08:121:37
HOMO SAPIENS (HUMAN).
Q03692

HRIFA007571a
ORM1 PROTEIN.
5.8e-17:106:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224

HRIFA007659a
HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
2.5e-47:213:41
CAENORHABDITIS ELEGANS.
P49191

HRIFA007722a
HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
7.7e-13:146:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857

HRIFA007728a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
9.1e-05:124:31
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

HRIFA007745a
ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (ACHE).
7.0e-15:109:36
TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).
P04058

HRIFA007829a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.00045:16:68
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157

HRIFA007909a
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
6.1e-06:173:34
BOS TAURUS (BOVINE).
P02453

HRIFA007985a

T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).
0.00079:97:37
ORYCTOLAGUS CUNICULUS (RABBIT).
P06333

HRIFA008000a
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR.
1.6e-37:165:42
ORYCTOLAGUS CUNICULUS (RABBIT).
P13806

HRIFA008174a
COLLAGEN 1(X) CHAIN PRECURSOR.
4.5e-05:215:28
BOS TAURUS (BOVINE).
P23206

HRIFA008186a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).
2.1e-25:118:46
HOMO SAPIENS (HUMAN).
P37058

HRIFA008200a
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
7.9e-17:139:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802

HRIFA008212a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
0.035:135:28
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

HRIFA008252a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
0.00015:128:32
MUS MUSCULUS (MOUSE).
P05142

HRIFA008284a
NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).
3.9e-18:153:30
HOMO SAPIENS (HUMAN).
P32004

HRIFA008314a
HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.
2.1e-18:99:47
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38800

HRIFA008362a
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).

9.1e-42:135:57
GALLUS GALLUS (CHICKEN).
P53760

HRIFA008426a
HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).
1.3e-08:104:45
GALLUS GALLUS (CHICKEN).
Q90655

HRIFA008459a
CARBON CATABOLITE DEREPRESSING PROTEIN KINASE (EC 2.7.1.-).
5.5e-15:96:40
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P06782

HRIFA008483a
PROBABLE LONG-CHAIN FATTY ACID TRANSPORT PROTEIN.
7.4e-26:154:41
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38225

HRIFA008547a
ZINC FINGER PROTEIN 136.
7.2e-57:228:50
HOMO SAPIENS (HUMAN).
P52737

HRIFA008596a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.6e-05:97:35
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA008611a
NPL1 PROTEIN (SEC63 PROTEIN).
8.1e-15:113:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14906

HRIFA008661a
GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).
2.7e-16:184:29
ESCHERICHIA COLI.
P37021

HRIFA008717a
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).
6.9e-32:198:41
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38692

HRIFA008784a
HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC REGION.
2.2e-16:93:47
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38869

HRIFA008790a
HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC REGION.
4.2e-08:121:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47111

HRIFA008976a
ACROSIN PRECURSOR (EC 3.4.21.10).
0.31:20:70
HOMO SAPIENS (HUMAN).
P10323

HRIFA008981a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.0e-84:126:74
HOMO SAPIENS (HUMAN).
Q03923

HRIFA008989a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
1.2e-05:134:33
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

HRIFA009071 a
CELLULAR TUMOR ANTIGEN P53 (PHOSPHOPROTEIN P53).
0.14:104:31
HOMO SAPIENS (HUMAN).
P04637

HRIFA009101a
ZINC FINGER PROTEIN 136.
6.5e-47:126:67
HOMO SAPIENS (HUMAN).
P52737

HRIFA009123a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.010:127:35
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA009136a
REGULATORY PROTEIN E2.
0.032:100:37
HUMAN PAPILLOMAVIRUS TYPE 25.
P36787

HRIFA009171a
BUTYROPHILIN PRECURSOR (BT).
1.6e-15:168:31
BOS TAURUS (BOVINE).
P18892

HRIFA009220a
HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I.
2.2e-48:268:41

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09895

HRIFA009339a
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.
0.63:57:35
MUS MUSCULUS (MOUSE).
Q01149

HRIFA009451a
METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES) (FIBROBLAST COLLAGENASE INHIBITOR) (COLLAGENASE INHIBITOR).
1.7e-57:163:73
HOMO SAPIENS (HUMAN).
P01033

HRIFA009482a
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
7.7e-25:86:59
MUS MUSCULUS (MOUSE).
P23780

HRIFA009578a
HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
8.8e-10:199:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857

HRIFA009762a
CCAAT DISPLACEMENT PROTEIN (CDP) (CDP2) (FRAGMENT).
0.17:116:32
RATTUS NORVEGICUS (RAT).
P53565

HRIFA009783a
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.
6.2e-48:231:48
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09782

HRIFA009825a
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
4.0e-06:70:38
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602

HRIFA009852a
"NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140]."
4.0e-07:198:27
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P16170

HRIFA009881a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
1.5e-11:106:35
SORGHUM VULGARE (SORGHUM).

P24152

HRIFA009983a
G-BOX BINDING FACTOR (GBF).
3.8e-10:156:30
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P36417

HRIFA010005a
"M PROTEIN, SEROTYPE 49 PRECURSOR."
1.6e-05:183:27
STREPTOCOCCUS PYOGENES.
P16947

HRIFA010078a
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
4.7e-05:194:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53214

HRIFA010085a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.9e-92:243:69
HOMO SAPIENS (HUMAN).
Q03923

HRIFA010090a
N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).
6.7e-16:78:51
HOMO SAPIENS (HUMAN).
P15586

HRIFA010130a
DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).
5.6e-13:99:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46971

HRIFA010152a
"ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE)."
2.3e-05:73:43
CANIS FAMILIARIS (DOG).
P30803

HRIFA010176a
HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B).
0.066:105:31
MUS MUSCULUS (MOUSE).
P35583

HRIFA010301a
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
1.1e-09:120:34
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602

HRIFA010319a
DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE) (DBH).
4.8e-23:185:32
RATTUS NORVEGICUS (RAT).
Q05754

HRIFA010361a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.6e-08:136:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA010394a
HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
3.3e-36:144:47
CAENORHABDITIS ELEGANS.
P49191

HRIFA010425a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.9e-09:199:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

HRIFA010460a
TRANSCRIPTIONAL ACTIVATOR FE65.
2.3e-27:101:54
RATTUS NORVEGICUS (RAT).
P46933

HRIFA010466a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
5.3e-07:123:34
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA010490a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (EARLY PROTEIN 0) (EP0).
0.0031:118:30
PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).
P29129

HRIFA010736a
PROTEIN Q300.
0.018:14:85
MUS MUSCULUS (MOUSE).
Q02722

HRIFA010790a
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).
1.6e-82:197:72
HOMO SAPIENS (HUMAN).
Q06495

HRIFA010799a

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
1.7e-05:220:30
GALLUS GALLUS (CHICKEN).
P02457

HRIFA010859a
ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR) (SUBTYPE C4).
0.063:134:33
HOMO SAPIENS (HUMAN).
P18825

HRIFA010891a
HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION.
0.044:28:64
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P36015

HRIFA010975a
TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).
8.5e-113:144:86
HOMO SAPIENS (HUMAN).
P43405

HRIFA010988a
GASTRIN PRECURSOR.
0.084:59:37
HOMO SAPIENS (HUMAN).
P01350

HRIFA011016a
PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) (CALCIUM-BINDING PROTEIN 2) (CABP2).
3.1e-15:127:37
RATTUS NORVEGICUS (RAT).
P38659

HRIFA011105a
SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.
0.97:41:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P02841

HRIFA011128a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.0046:30:63
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157

HRIFA011179a
PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-).
1.1e-20:127:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P34244

HRIFA011197a
DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).
5.8e-26:169:40
MUS MUSCULUS (MOUSE).

P28843

HRIFA011449a
GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P58/GTA (EC 2.7.1.-).
1.9e-26:109:53
MUS MUSCULUS (MOUSE).
P24788

HRIFA011484a
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.00055:115:33
HOMO SAPIENS (HUMAN).
P21917

HRIFA011512a
POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).
0.00024:139:25
HOMO SAPIENS (HUMAN).
P51531

HRIFA011580a
VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI) PHOSVITIN (PV) LIPOVITELLIN II (LVII) YGP40].
4.0e-08:182:32
GALLUS GALLUS (CHICKEN).
P02845

HRIFA011659a
VON WILLEBRAND FACTOR PRECURSOR.
9.8e-17:210:25
HOMO SAPIENS (HUMAN).
P04275

HRIFA011820a
ZINC FINGER PROTEIN 136.
1.9e-10:42:73
HOMO SAPIENS (HUMAN).
P52737

HRIFA011926a
TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).
1.0:149:22
PSEUDOMONAS AERUGINOSA.
P15276

HRIFA011947a
ZINC FINGER PROTEIN 136.
1.3e-80:180:72
HOMO SAPIENS (HUMAN).
P52737

HRIFA012069a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
0.0027:205:28
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

HRIFA012151a

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.
0.00028:72:37
RATTUS NORVEGICUS (RAT).
Q07008

HRIFA012167a
HYPOTHETICAL SYMPORTER IN GLTS-SELC INTERGENIC REGION.
6.4e-09:145:28
ESCHERICHIA COLI.
P31435

HRIFA012278a
ZINC FINGER PROTEIN 140.
3.1e-14:88:52
HOMO SAPIENS (HUMAN).
P52738

HRIFA012354a
"SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT."
2.1e-05:120:32
RATTUS NORVEGICUS (RAT).
P04775

HRIFA012427a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
6.3e-08:250:28
MUS MUSCULUS (MOUSE).
P11087

HRIFA012436a
INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).
4.7e-09:95:31
HOMO SAPIENS (HUMAN).
Q04941

HRIFA012515a
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).
3.5e-06:181:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170

HRIFA012584a
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).
4.9e-14:136:29
NEUROSPORA CRASSA.
P23231

HRIFA012625a
"HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT)."
9.6e-12:103:40
RATTUS NORVEGICUS (RAT).
P13386

HRIFA012692a

BLOOM'S SYNDROME PROTEIN.
6.3e-26:203:34
HOMO SAPIENS (HUMAN).
P54132

HRIFA012702a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
1.9e-07:153:30
ZEA MAYS (MAIZE).
P14918

HRIFA012737a
LEUCOCYTE ANTIGEN CD97 PRECURSOR.
1.6e-09:170:24
HOMO SAPIENS (HUMAN).
P48960

HRIFA012795a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).
3.0e-34:189:39
RATTUS NORVEGICUS (RAT).
P15387

HRIFA012885a
HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.
2.9e-21:159:40
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47032

HRIFA012914a
ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70 TRANSMEMBRANE PROTEIN P20E].
3.4e-29:134:47
BABOON ENDOGENOUS VIRUS (STRAIN M7).
P10269

HRIFA012969a
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
1.2e-30:228:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802

HRIFA012990a
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
7.4e-20:181:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986

HRIFA013092a
OUTER MEMBRANE PROTEIN H.8 PRECURSOR.
0.0039:51:39
NEISSERIA GONORRHOEAE.
P11910

HRIFA013103a
N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANS-

FERASE) (GT).
0.25:50:34
MUS MUSCULUS (MOUSE).
P15535

HRIFA013135a
CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1).
1.6e-05:214:28
CLOSTRIDIUM THERMOCELLUM.
Q06852

HRIFA013235a
PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.
1.9e-05:113:40
HOMO SAPIENS (HUMAN).
P02461

HRIFA013254a
COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].
3.8e-13:123:41
MUS MUSCULUS (MOUSE).
P01029

HRIFA013265a
CATHEPSIN L PRECURSOR (EC 3.4.22.15) (MAJOR EXCRETED PROTEIN) (MEP).
7.0e-107:225:86
HOMO SAPIENS (HUMAN).
P07711

HRIFA013276a
5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).
2.2e-117:270:85
HOMO SAPIENS (HUMAN).
P21589

HRIFA013279a
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
4.9e-05:127:37
PLASMODIUM VIVAX.
P08677

HRIFA013376a
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).
8.0e-23:230:31
NEUROSPORA CRASSA.
P23231

HRIFA013477a
OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).
5.8e-87:197:87
HOMO SAPIENS (HUMAN).
P41217

HRIFA013586a
ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

3.8e-31:93:64
BOS TAURUS (BOVINE).
P07106

HRIFA013589a
T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).
5.0e-06:95:35
HOMO SAPIENS (HUMAN).
P40200

HRIFA013620a
"HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT)."
7.1e-08:95:37
MUS MUSCULUS (MOUSE).
P20490

HRIFA013726a
SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).
1.5e-33:99:50
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q03497

HRIFA013744a
ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).
7.5e-15:105:38
BOS TAURUS (BOVINE).
P07106

HRIFA013911a
BIOTINIDASE PRECURSOR (EC 3.5.1.12).
7.8e-37:104:46
HOMO SAPIENS (HUMAN).
P43251

HRIFA013919a
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
1.2e-10:170:32
HOMO SAPIENS (HUMAN).
Q02817

HRIFA013932a
"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6" PEPTIDE P-H].
2.6e-05:168:34
HOMO SAPIENS (HUMAN).
P04280

HRIFA013980a
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).
0.00036:157:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P18480

HRIFA014006a
T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).

9.4e-16:185:28
MUS MUSCULUS (MOUSE).
P20937

HRIFA014024a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.0013:102:44
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128

HRIFA014056a
PROTEIN Q300.
5.1e-05:24:70
MUS MUSCULUS (MOUSE).
Q02722

HRIFA014111a
TOLL PROTEIN PRECURSOR.
5.5e-08:203:27
DROSOPHILA MELANOGASTER (FRUIT FLY).
P08953

HRIFA014133a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.6e-06:143:33
MUS MUSCULUS (MOUSE).
P05142

HRIFA014185a
LEUCOCYTE ANTIGEN CD97 PRECURSOR.
6.0e-14:192:30
HOMO SAPIENS (HUMAN).
P48960

HRIFA014336a
"GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (FRAGMENT)."
2.8e-70:198:58
SUS SCROFA (PIG).
P20305

HRIFA014396a
CREB-BINDING PROTEIN.
2.6e-07:101:34
MUS MUSCULUS (MOUSE).
P45481

HRIFA014397a
GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.
5.2e-05:147:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25655

HRIFA014465a
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
2.8e-11:166:30
CAENORHABDITIS ELEGANS.
P30638

HRIFA014500a
HYPOTHETICAL 71.4 KD PROTEIN IN NMD3-ENO2 INTERGENIC REGION.
1.0e-14:149:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38862

HRIFA014561a
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR1.
4.1e-70:156:89
HOMO SAPIENS (HUMAN).
P46091

HRIFA014568a
AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE).
2.4e-40:196:44
RATTUS NORVEGICUS (RAT).
P15684

HRIFA014590a
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
0.18:26:30
GALLUS GALLUS (CHICKEN).
P14093

HRIFA014598a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
4.9e-05:124:29
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA014620a
ENL PROTEIN.
0.58:170:30
HOMO SAPIENS (HUMAN).
Q03111

HRIFA014621a
PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.
2.7e-50:150:74
HOMO SAPIENS (HUMAN).
P11462

HRIFA014688a
INTEGRIN BETA-6 SUBUNIT PRECURSOR.
6.9e-31:189:39
HOMO SAPIENS (HUMAN).
P18564

HRIFA014702a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
6.4e-05:89:40
MUS MUSCULUS (MOUSE).
P05142

HRIFA014819a
MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.
7.8e-26:117:46
HOMO SAPIENS (HUMAN).

P55083

HRIFA014868a
SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
8.9e-08:195:29
DROSOPHILA ERECTA (FRUIT FLY).
P13730

HRIFA014951a
PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).
4.1e-23:132:39
EQUUS CABALLUS (HORSE).
P80010

HRIFA014967a
CHLORINE CHANNEL PROTEIN P64.
2.0e-52:142:76
BOS TAURUS (BOVINE).
P35526

HRIFA015063a
ZINC FINGER PROTEIN 136.
6.6e-53:229:48
HOMO SAPIENS (HUMAN).
P52737

HRIFA015070a
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).
9.3e-24:143:41
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38692

HRIFA015122a
REGULATORY PROTEIN E2.
0.45:129:30
HUMAN PAPILLOMAVIRUS TYPE 5.
P06921

HRIFA015219a
FIBRILLIN 1 PRECURSOR (MP340).
9.9e-09:132:32
BOS TAURUS (BOVINE).
P98133

HRIFA015246a
PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 4 PRECURSOR (PSBG-4).
2.4e-33:184:46
HOMO SAPIENS (HUMAN).
Q00888

HRIFA015351a
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
0.0021:122:30
RATTUS NORVEGICUS (RAT).
P03994

HRIFA015423a
B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).

1.2e-11:148:35
HOMO SAPIENS (HUMAN).
P20749

HRIFA015453a
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
6.8e-11:91:37
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P54644

HRIFA015486a
BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR).
2.0e-22:208:27
MUS MUSCULUS (MOUSE).
Q01339

HRIFA015506a
COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).
1.3e-12:73:50
HOMO SAPIENS (HUMAN).
P23508

HRIFA015536a
CHLORINE CHANNEL PROTEIN P64.
1.2e-49:115:79
BOS TAURUS (BOVINE).
P35526

HRIFA015547a
BEM46 PROTEIN (FRAGMENT).
1.4e-33:137:49
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P54069

HRIFA015568a
HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.
2.4e-16:152:34
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09875

HRIFA015756a
EBNA-2 NUCLEAR PROTEIN.
2.9e-15:28:75
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P12978

HRIFA015802a
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
0.0035:122:30
RATTUS NORVEGICUS (RAT).
P03994

HRIFA015811a
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
6.2e-39:171:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

HRIFA015902a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
0.0075:161:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

HRIFA015947a
ZINC FINGER Y-CHROMOSOMAL PROTEIN 1.
0.035:98:28
MUS MUSCULUS (MOUSE).
P10925

HRIFA015995a
PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.
6.2e-08:221:37
HOMO SAPIENS (HUMAN).
P02461

HRIFA016070a
"COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR."
1.0e-18:179:35
HOMO SAPIENS (HUMAN).
P02745

HRIFA016214a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
4.0e-05:96:42
MUS MUSCULUS (MOUSE).
P05142

HRIFA016240a
HYPOTHETICAL 65.3 KD PROTEIN IN PRE3-SAG1 INTERGENIC REGION.
8.5e-05:103:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47082

HRIFA016255a
EBNA-1 NUCLEAR PROTEIN.
4.5e-09:219:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA016290a
COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).
6.7e-21:182:41
HOMO SAPIENS (HUMAN).
P12259

HRIFA016430a
ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1).
7.1e-50:120:86
HOMO SAPIENS (HUMAN).
P24390

HRIFA016599a
MEIOTIC RECOMBINATION PROTEIN REC104.
0.57:73:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P33323

HRIFA016639a
"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."
8.0e-06:206:23
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640

HRIFA016654a
HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).
1.1e-78:181:86
ORYCTOLAGUS CUNICULUS (RABBIT).
P33279

HRIFA016669a
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
1.4e-08:87:36
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602

HRIFA016758a
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
9.5e-17:158:40
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

HRIFA016963a
FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR.
6.2e-08:131:32
LYMNAEA STAGNALIS (GREAT POND SNAIL).
P42565

HRIFA017031a
MYOSIN HEAVY CHAIN KINASE A (EC 2.7.1.129) (MHCK A).
2.6e-11:152:34
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P42527

HRIFA017146a
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.0014:78:37
HOMO SAPIENS (HUMAN).
P21917

HRIFA017190a
FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).
0.0026:89:30
HOMO SAPIENS (HUMAN).
Q01543

HRIFA017257a
"GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL)."
2.5e-79:261:57
HOMO SAPIENS (HUMAN).
P06396

HRIFA017295a

"ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II)."
3.4e-20:66:78
HOMO SAPIENS (HUMAN).
Q10469

HRIFA017312a
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN) (PRP).
2.7e-19:221:33
HOMO SAPIENS (HUMAN).
P04003

HRIFA017456a
LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).
0.11:94:35
MUS MUSCULUS (MOUSE).
P19137

HRIFA017457a
SYNAPTOTAGMIN II.
7.2e-07:98:35
MUS MUSCULUS (MOUSE).
P46097

HRIFA017643a
NOV PROTEIN HOMOLOG PRECURSOR (NOVH).
2.2e-07:81:41
HOMO SAPIENS (HUMAN).
P48745

HRIFA017670a
TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.
4.9e-06:172:27
RATTUS NORVEGICUS (RAT).
P19814

HRIFA017703a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
1.9e-16:129:34
THERMOMONOSPORA CURVATA.
P49695

HRIFA017791a
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
0.012:71:38
HOMO SAPIENS (HUMAN).
Q02817

HRIFA017801a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
4.5e-07:86:39
MUS MUSCULUS (MOUSE).
P05142

HRIFA017818a
ATP SYNTHASE C CHAIN (EC 3.6.1.34) (LIPID-BINDING PROTEIN).
1.0:32:40

STREPTOMYCES LIVIDANS.
P50014

HRIFA017836a
"TETRACYCLINE RESISTANCE PROTEIN, CLASS H (TETA(H))."
1.3e-08:113:31
PASTEURELLA MULTOCIDA.
P51564

HRIFA017855a
ORM1 PROTEIN.
1.7e-18:137:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224

HRIFA017921a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
2.0e-09:182:35
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

HRIFA018092a
"DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2-DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT)."
2.1e-20:119:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P17898

HRIFA018131a
ORM1 PROTEIN.
2.6e-20:137:37
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224

HRIFA018134a
SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).
1.1e-11:147:32
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
Q05609

HRIFA018238a
NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).
8.6e-06:74:44
MUS MUSCULUS (MOUSE).
Q01705

HRIFA018262a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
6.4e-10:71:38
THERMOMONOSPORA CURVATA.
P49695

HRIFA018287a
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
1.5e-06:214:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53214

HRIFA018447a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.00065:133:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA018580a
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
2.1e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020

HRIFA018666a
PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE PHOSPHOHYDROLASE).
1.7e-06:191:28
DROSOPHILA MELANOGASTER (FRUIT FLY).
P16621

HRIFA018688a
PHLB PROTEIN PRECURSOR.
1.9e-06:110:35
SERRATIA LIQUEFACIENS.
P18954

HRIFA018754a
"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."
1.8e-06:195:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640

HRIFA018794a
MSP1 PROTEIN HOMOLOG.
3.2e-06:93:25
CAENORHABDITIS ELEGANS.
P54815

HRIFA018827a
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
3.1e-17:180:28
CAENORHABDITIS ELEGANS.
P30638

HRIFA018870a
HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.
4.7e-09:70:37
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47088

HRIFA018904a
MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DISTROPHY PROTEIN KINASE) (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).
5.5e-12:142:32
HOMO SAPIENS (HUMAN).
Q09013

HRIFA018931a

ZINC FINGER PROTEIN 140.
2.9e-10:47:74
HOMO SAPIENS (HUMAN).
P52738

HRIFA018993a
HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.
1.2e-13:117:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53073

HRIFA019105a
DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).
7.5e-22:203:32
DROSOPHILA MELANOGASTER (FRUIT FLY).
P25723

HRIFA019136a
"MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L PROTEIN)."
1.0e-25:74:81
HOMO SAPIENS (HUMAN).
P29966

HRIFA019175a
PROTEIN KINASE WIS1 (EC 2.7.1.-).
1.3e-14:84:39
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P33886

HRIFA019262a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.5e-55:188:50
HOMO SAPIENS (HUMAN).
Q03923

HRIFA019412a
CATHEPSIN E PRECURSOR (EC 3.4.23.34).
1.4e-09:121:33
CAVIA PORCELLUS (GUINEA PIG).
P25796

HRIFA019437a
REGULATORY PROTEIN E2.
0.26:77:37
HUMAN PAPILLOMAVIRUS TYPE 14.
P36783

HRIFA019466a
EBNA-1 NUCLEAR PROTEIN.
2.7e-19:130:43
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA019490a
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).
1.1e-09:132:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P18480

HRIFA019498a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAL (SHAL2).
5.6e-05:87:36
DROSOPHILA MELANOGASTER (FRUIT FLY).
P17971

HRIFA019532a
EBNA-1 NUCLEAR PROTEIN.
1.8e-05:67:49
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA019651a
ACIDIC PHOSPHOPROTEIN PRECURSOR (50 KD ANTIGEN).
6.1e-05:31:64
PLASMODIUM CHABAUDI.
Q02752

HRIFA019867a
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).
8.2e-34:103:71
RATTUS NORVEGICUS (RAT).
Q06496

HRIFA019869a
SERINE/THREONINE-PROTEIN KINASE FUSED (EC 2.7.1.-).
7.2e-29:83:49
DROSOPHILA MELANOGASTER (FRUIT FLY).
P23647

HRIFA019958a
REPRESSOR PROTEIN CI (FRAGMENT).
0.99:45:37
BACTERIOPHAGE 434.
P16117

HRIFA020144a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.8e-06:176:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA020184a
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
1.9e-10:102:37
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P18160

HRIFA020272a
MUSCARINIC ACETYLCHOLINE RECEPTOR M3.
5.5e-91:211:85
HOMO SAPIENS (HUMAN).
P20309

HRIFA020335a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
5.0e-104:275:72
HOMO SAPIENS (HUMAN).
P27448

HRIFA020349a
BRITTLE-1 PROTEIN PRECURSOR.
6.0e-30:214:35
ZEA MAYS (MAIZE).
P29518

HRIFA020453a
PROTEIN TRANSPORT PROTEIN SEC22 (PROTEIN SLY2).
2.5e-08:132:28
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22214

HRIFA020693a
TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).
3.9e-09:96:35
HOMO SAPIENS (HUMAN).
P43146

HRIFA020707a
PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PSSA-1).
3.4e-09:95:33
TRYPANOSOMA BRUCEI BRUCEI.
Q06084

HRIFA020748a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
3.2e-09:210:28
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

HRIFA020862a
MODIFIER 3 PROTEIN (M33).
5.6e-26:76:61
MUS MUSCULUS (MOUSE).
P30658

HRIFA020883a
PROTEIN Q300.
0.00054:21:66
MUS MUSCULUS (MOUSE).
Q02722

HRIFA021007a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
0.092:73:36
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)
P08393

HRIFA021040a
TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).

0.98:63:39
HOMO SAPIENS (HUMAN).
P43694

HRIFA021061a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.8e-09:162:31
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA021213a
OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.
2.0e-38:96:72
CAENORHABDITIS ELEGANS.
P46975

HRIFA021224a
RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).
2.8e-06:55:52
RATTUS NORVEGICUS (RAT).
Q02975

HRIFA021398a
COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).
2.5e-17:78:51
ORYCTOLAGUS CUNICULUS (RABBIT).
P98139

HRIFA021445a
PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-1 (HOMEOBOX PROTEIN PBX1) (HOMEOBOX PROTEIN PRL).
0.38:146:31
HOMO SAPIENS (HUMAN).
P40424

HRIFA021494a
EBNA-1 NUCLEAR PROTEIN.
6.8e-07:116:41
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA021499a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
7.1e-34:159:50
GALLUS GALLUS (CHICKEN).
P05099

HRIFA021543a
ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).
0.0087:50:40
GALLUS GALLUS (CHICKEN).
Q03352

HRIFA021620a
PLATELET FACTOR 4 (PF-4).
0.019:65:27
SUS SCROFA (PIG).
P30034

HRIFA021637a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
6.0e-37:147:53
GALLUS GALLUS (CHICKEN).
P05099

HRIFA021651a
CARG-BINDING FACTOR-A (CBF-A).
2.6e-11:170:30
MUS MUSCULUS (MOUSE).
Q99020

HRIFA021754a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
1.2e-37:137:51
GALLUS GALLUS (CHICKEN).
P05099

HRIFA021781a
DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2).
7.1e-19:199:31
HOMO SAPIENS (HUMAN).
P18074

HRIFA021787a
PROTEIN Q300.
0.051:13:84
MUS MUSCULUS (MOUSE)
Q02722

HRIFA021794a
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
1.6e-07:90:32
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P54644

HRIFA021855a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
8.6e-06:163:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA021906a
S-ANTIGEN PROTEIN PRECURSOR.
2.1e-09:226:28
PLASMODIUM FALCIPARUM (ISOLATE V1).
P09593

HRIFA022055a
BETA-LYTIC METALLOENDOPEPTIDASE PRECURSOR (EC 3.4.24.32) (BETA-LYTIC PROTEASE).
0.63:118:31
ACHROMOBACTER LYTICUS.
P27458

HRIFA022065a
BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR.
9.7e-24:235:34

HOMO SAPIENS (HUMAN).
P16279

HRIFA022139a
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.
2.1e-57:232:52
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09782

HRIFA022156a
"GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR."
1.4e-07:133:35
TRITICUM AESTIVUM (WHEAT).
P08489

HRIFA022166a
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).
3.5e-28:194:35
HOMO SAPIENS (HUMAN).
Q03468

HRIFA022177a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
2.2e-12:137:32
THERMOMONOSPORA CURVATA.
P49695

HRIFA022182a
SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1 -) (MALE GERM CELL-ASSOCIATED KINASE).
1.2e-47:121:79
RATTUS NORVEGICUS (RAT).
P20793

HRIFA022203a
COLLAGEN ALPHA 1 (III) CHAIN.
1.1e-05:211:33
BOS TAURUS (BOVINE).
P04258

HRIFA022227a
POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1) (PPSEP 1).
3.2e-31:229:36
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10071

HRIFA022234a
CARBOXYPEPTIDASE KEX1 PRECURSOR (EC 3.4.16.6) (CARBOXYPEPTIDASE D).
1.8e-08:110:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P09620

HRIFA022249a
ZINC FINGER PROTEIN 133.
1.1e-34:84:48
HOMO SAPIENS (HUMAN).
P52736

HRIFA022265a
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN (EC 2.7.1.123) (CAM KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].
5.1e-26:188:40
RATTUS NORVEGICUS (RAT).
P13234

HRIFA022328a
SCO1 PROTEIN PRECURSOR.
5.4e-25:84:45
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23833

HRIFA022335a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
0.21:121:29
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

HRIFA022348a
AGAMOUS PROTEIN.
1.0 40:42
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P17839

HRIFA022411a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
0.00059:111:35
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

HRIFA022423a
HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
2.5e-15:106:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857

HRIFA022462a
RETINOIC ACID RECEPTOR RXR-BETA.
0.0010:124:33
HOMO SAPIENS (HUMAN).
P28702

HRIFA022493a
ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).
0.0018:130:34
MUS MUSCULUS (MOUSE).
Q01338

HRIFA022528a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
3.2e-23:230:28
ZEA MAYS (MAIZE).
P14918

HRIFA022546a

NINAC SHORT PROTEIN (EC 2.7.1.-).
8.5e-42:209:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P10677

HRIFA022564a
ZINC FINGER PROTEIN 140.
7.9e-23:116:51
HOMO SAPIENS (HUMAN).
P52738

HRIFA022616a
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91).
7.4e-36:172:43
HOMO SAPIENS (HUMAN).
Q07954

HRIFA022671a
PAIRED AMPHIPATHIC HELIX PROTEIN.
2.0e-26:186:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579

HRIFA022691a
FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREP-A).
1.4e-44:229:41
PARASTICHOPUS PARVIMENSIS (SEA CUCUMBER).
P19477

HRIFA022702a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
1.1e-08:146:38
GALLUS GALLUS (CHICKEN).
P02457

HRIFA022707a
GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9) (TCF-9).
7.0e-40:229:37
HOMO SAPIENS (HUMAN).
P16383

HRIFA022714a
"AMELOGENIN, CLASS I PRECURSOR."
0.62:96:31
BOS TAURUS (BOVINE).
P02817

HRIFA022728a
ACROSIN PRECURSOR (EC 3.4.21.10) (53 KD FUCOSE-BINDING PROTEIN).
1.7e-06:28:64
SUS SCROFA (PIG).
P08001

HRIFA022729a
"ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II) "

7.7e-29:69:84
HOMO SAPIENS (HUMAN).
Q10469

HRIFA022737a
TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225).
6.7e-19:170:37
GALLUS GALLUS (CHICKEN).
P10039

HRIFA022776a
PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).
4.0e-20:199:31
MEDICAGO SATIVA (ALFALFA).
P38661

HRIFA022782a
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
3.7e-09:184:36
PLASMODIUM CYNOMOLGI (STRAIN BEROK).
P08672

HRIFA022865a
COLLAGEN ALPHA 1(III) CHAIN.
2.5e-09:169:33
BOS TAURUS (BOVINE).
P04258

HRIFA022875a
BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).
9.1e-14:115:33
BOS TAURUS (BOVINE).
P21793

HRIFA022890a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.8e-10:237:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA022895a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.4e-106:283:67
HOMO SAPIENS (HUMAN).
Q03923

HRIFA022985a
PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PSSA-1).
3.0e-10:33:72
TRYPANOSOMA BRUCEI BRUCEI.
Q06084

HRIFA023007a
MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).
1.1e-27:66:54
HOMO SAPIENS (HUMAN).

P22670

HRIFA023048a
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
2.2e-07:221:33
RATTUS NORVEGICUS (RAT).
P02454

HRIFA023069a
BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).
3.4e-08:149:31
HOMO SAPIENS (HUMAN).
P98160

HRIFA023129a
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
4.2e-06:37:51
PLASMODIUM LOPHURAE.
P04929

HRIFA023154a
GLYCOPROTEIN X PRECURSOR.
8.2e-05:140:27
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

HRIFA023212a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
8.3e-10:249:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

HRIFA023227a
GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).
9.2e-15:180:30
ESCHERICHIA COLI.
P37021

HRIFA023257a
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
2.4e-118:229:88
RATTUS NORVEGICUS (RAT).
P38378

HRIFA023304a
PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA2+-ATPASE).
1.3e-23:222:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39524

HRIFA023434a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).
0.00018:157:30
RATTUS NORVEGICUS (RAT).
P17659

HRIFA023464a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.0e-11:75:46
ORYZA SATIVA (RICE).
P29834

HRIFA023489a
HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.
4.4e-09:230:23
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10297

HRIFA023634a
EBNA-1 NUCLEAR PROTEIN.
1.8e-08:113:45
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA023767a
CYTOCHROME B5.
1.1e-12:92:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40312

HRIFA023894a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.6e-05:80:40
MUS MUSCULUS (MOUSE).
P05142

HRIFA023923a
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
4.2e-76:128:85
HOMO SAPIENS (HUMAN).
P00395

HRIFA024088a
NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).
1.1e-05:118:32
MUS MUSCULUS (MOUSE).
P98084

HRIFA024132a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.9.
6.5e-40:136:61
HOMO SAPIENS (HUMAN).
P51787

HRIFA024185a
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
0.55:128:29
HOMO SAPIENS (HUMAN).
P50548

HRIFA024197a
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP (CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).

7.5e-09:93:34
NEUROSPORA CRASSA.
P23231

HRIFA024218a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
6.7e-06:180:36
HOMO SAPIENS (HUMAN).
P02452

HRIFA024255a
HYPOTHETICAL 116.3 KD PROTEIN C26F1.09 IN CHROMOSOME I.
4.8e-23:172:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
O10496

HRIFA024305a
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).
0.047:47:29
HOMO SAPIENS (HUMAN).
P18850

HRIFA024392a
TRANSMEMBRANE PROTEIN SEX PRECURSOR.
6.7e-24:119:43
HOMO SAPIENS (HUMAN).
P51805

HRIFA024423a
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
2.1e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020

HRIFA024473a
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
3.3e-05:106:41
BOS TAURUS (BOVINE).
P02453

HRIFA024482a
PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).
1.2e-07:99:31
NICOTIANA TABACUM (COMMON TOBACCO)
O03211

HRIFA024504a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).
2.6e-43:205:49
HOMO SAPIENS (HUMAN).
P37058

HRIFA024543a
GLYCOPROTEIN X PRECURSOR.
1.5e-06:257:28
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

HRIFA024718a
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
5.3e-45:168:52
MUS MUSCULUS (MOUSE).
P23780

HRIFA024767a
SODIUM CHANNEL PROTEIN (NA+ CHANNEL).
7.4e-30:221:31
ELECTROPHORUS ELECTRICUS (ELECTRIC EEL).
P02719

HRIFA024884a
HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.
0.0089:23:65
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53245

HRIFA024893a
REGULATORY PROTEIN E2.
0.0021:167:31
HUMAN PAPILLOMAVIRUS TYPE 8.
P06422

HRIFA024937a
GNS1 PROTEIN.
1.0e-15:173:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25358

HRIFA024978a
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
0.00019:150:32
HOMO SAPIENS (HUMAN).
Q02817

HRIFA024994a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
5.3e-22:145:46
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

HRIFA025033a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
0.50:215:29
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284

HRIFA025046a
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
1.7e-41:104:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986

HRIFA025250a
PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)).
7.4e-17:126:34
DROSOPHILA MELANOGASTER (FRUIT FLY).

P05130

HRIFA025261a
MYOSIN I ALPHA (MMI-ALPHA).
2.3e-64:141:84
MUS MUSCULUS (MOUSE).
P46735

HRIFA025290a
EBNA-1 NUCLEAR PROTEIN.
0.016:79:40
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA025327a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
2.3e-06:104:37
MUS MUSCULUS (MOUSE).
P05142

HRIFA025353a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.0e-11:75:46
ORYZA SATIVA (RICE).
P29834

HRIFA025479a
PROTEASE DEGS PRECURSOR (EC 3.4.21.-).
3.0e-05:112:33
ESCHERICHIA COLI.
P31137

HRIFA025488a
PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR (FRAGMENTS).
9.5e-05:104:40
MUS MUSCULUS (MOUSE).
P08121

HRIFA025492a
SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK).
1.8e-53:159:69
HOMO SAPIENS (HUMAN).
Q13627

HRIFA025636a
MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 (EC 3.4.24.-) (TAT-BINDING HOMOLOG 12).
4.7e-32:81:66
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40341

HRIFA025695a
PEREGRIN (BR140 PROTEIN).
3.1e-40:227:43
HOMO SAPIENS (HUMAN).
P55201

HRIFA025703a

CELL SURFACE ANTIGEN 114/A10 PRECURSOR.
1.8e-08:71:42
MUS MUSCULUS (MOUSE).
P19467

HRIFA025706a
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
1.2e-28:111:44
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

HRIFA025766a
CYTOCHROME B5.
4.2e-13:133:33
ORYCTOLAGUS CUNICULUS (RABBIT).
P00169

HRIFA025771a
HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.
6.7e-10:129:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53288

HRIFA025778a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.5e-05:212:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

HRIFA025800a
HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.
3.7e-18:165:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40544

HRIFA025904a
COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).
2.6e-05:211:28
HOMO SAPIENS (HUMAN).
P17927

HRIFA025907a
INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR (IGUPI-5111).
2.1e-38:176:38
HOMO SAPIENS (HUMAN).
Q06323

HRIFA025913a
DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).
2.5e-32:185:37
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46971

HRIFA025936a
TRANSCRIPTIONAL ACTIVATOR FE65.
3.4e-09:43:46
RATTUS NORVEGICUS (RAT).
P46933

HRIFA025966a
SYNAPTOTAGMIN III.
4.5e-05:93:33
RATTUS NORVEGICUS (RAT).
P40748

HRIFA025978a
"GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DX5 PRECURSOR."
3.5e-06:224:28
TRITICUM AESTIVUM (WHEAT).
P10388

HRIFA026089a
BUTYROPHILIN PRECURSOR (BT).
1.1e-12:146:29
BOS TAURUS (BOVINE).
P18892

HRIFA026121a
FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
9.7e-06:72:43
HOMO SAPIENS (HUMAN).
P48023

HRIFA026242a
HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.
7.4e-09:188:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P48566

HRIFA026265a
DNA BINDING PROTEIN S1FA.
0.67:43:37
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P42551

HRIFA026303a
SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).
0.014:88:32
HOMO SAPIENS (HUMAN).
P10163

HRIFA026316a
EBNA-2 NUCLEAR PROTEIN.
1.5e-07:82:35
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P12978

HRIFA026351a
FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).
0.019:89:31
HOMO SAPIENS (HUMAN).
Q01543

HRIFA026364a
PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1
8.3e-40:167:49
RATTUS NORVEGICUS (RAT).

P48303

HRIFA026382a
T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).
6.2e-10:135:38
ORYCTOLAGUS CUNICULUS (RABBIT).
P06333

HRIFA026465a
COLLAGEN ALPHA 1(IX) CHAIN PRECURSOR (FRAGMENTS).
8.6e-07:158:35
GALLUS GALLUS (CHICKEN).
P12106

HRIFA026496a
ZINC FINGER PROTEIN 140.
5.9e-24:122:52
HOMO SAPIENS (HUMAN).
P52738

HRIFA026519a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.3e-08:130:36
MUS MUSCULUS (MOUSE).
P05142

HRIFA026564a
GLYCOPROTEIN X PRECURSOR
1.8e-10:225:25
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

HRIFA026576a
ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
1.7e-09:116:34
HOMO SAPIENS (HUMAN).
P12235

HRIFA026615a
REGULATORY PROTEIN E2.
0.0024:132:31
HUMAN PAPILLOMAVIRUS TYPE 9.
P36780

HRIFA026618a
PROTEIN Q300.
1.2e-05:27:66
MUS MUSCULUS (MOUSE).
Q02722

HRIFA026659a
SERINE/THREONINE-PROTEIN KINASE SGK (EC 2.7.1.-) (SERUM/GLUCOCORTICOID-REGULATED KINASE).
2.0e-10:81:45
RATTUS NORVEGICUS (RAT).
Q06226

HRIFA026764a
MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1) (CD48).
3.4e-05:162:25
RATTUS NORVEGICUS (RAT).
P10252

HRIFA026789a
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.
8.1e-22:175:38
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09818

HRIFA026813a
"PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU)."
7.1e-89:256:67
HOMO SAPIENS (HUMAN).
Q15139

HRIFA026860a
MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).
2.6e-19:103:43
MESOCRICETUS AURATUS (GOLDEN HAMSTER).
P53988

HRIFA026923a
CCAAT DISPLACEMENT PROTEIN (HOMEOBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).
0.18:119:36
CANIS FAMILIARIS (DOG).
P39881

HRIFA027012a
"MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (ALPHA-MANNOSIDASE 1A)."
1.8e-44:234:41
MUS MUSCULUS (MOUSE).
P45700

HRIFA027045a
HYPOTHETICAL PROTEIN HI0519.
2.7e-27:181:38
HAEMOPHILUS INFLUENZAE.
P44742

HRIFA027125a
ZINC FINGER PROTEIN 133.
3.9e-33:70:61
HOMO SAPIENS (HUMAN).
P52736

HRIFA027173a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
0.15:137:27
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284

HRIFA027179a
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).
3.6e-30:90:77

HOMO SAPIENS (HUMAN).
Q03468

HRIFA027187a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
4.7e-11:44:61
HOMO SAPIENS (HUMAN).
P20931

HRIFA027327a
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
3.8e-07:184:35
HOMO SAPIENS (HUMAN).
Q03692

HRIFA027329a
SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
9.1e-08:195:29
DROSOPHILA ERECTA (FRUIT FLY).
P13730

HRIFA027355a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
1.9e-06:33:72
HOMO SAPIENS (HUMAN).
P20931

HRIFA027485a
COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR.
0.00099:174:36
HOMO SAPIENS (HUMAN).
P12107

HRIFA027536a
VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).
0.0042:104:35
DROSOPHILA MELANOGASTER (FRUIT FLY).
P13238

HRIFA027549a
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.00023:101:44
HOMO SAPIENS (HUMAN).
P21917

HRIFA027622a
GUANOSINE-DIPHOSPHATASE (EC 3.6.1.42) (GDPASE).
2.2e-23:146:45
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32621

HRIFA027625a
CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).
1.1e-57:220:54
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P13586

HRIFA027644a

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
7.5e-05:72:40
RATTUS NORVEGICUS (RAT).
P02454

HRIFA027656a
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
1.6e-13:149:34
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P18160

HRIFA027673a
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
6.4e-06:47:57
HOMO SAPIENS (HUMAN).
P29279

HRIFA027681a
SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).
1.1e-13:158:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08458

HRIFA027714a
HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN CHROMOSOME III.
7.2e-06:146:30
CAENORHABDITIS ELEGANS.
P46580

HRIFA027722a
SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).
2.7e-105:242:85
CANIS FAMILIARIS (DOG).
Q00004

HRIFA027860a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
8.3e-08:168:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA027867a
STANNIOCALCIN PRECURSOR (STC) (CORPUSCLES OF STANNIUS PROTEIN) (CS) (HYPOCALCIN) (TELEOCALCIN).
1.0:100:27
ANGUILLA AUSTRALIS (AUSTRALIAN EEL).
P18301

HRIFA027940a
INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
8.7e-15:149:38
HOMO SAPIENS (HUMAN).
P55103

HRIFA028061a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
9.7e-07:157:26
THERMOMONOSPORA CURVATA

P49695

HRIFA028157a
HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).
2.8e-71:201:68
HOMO SAPIENS (HUMAN).
P30825

HRIFA028187a
EBNA-1 NUCLEAR PROTEIN.
1.5e-09:131:38
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA028262a
CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).
7.2e-09:99:33
MUS MUSCULUS (MOUSE).
P53996

HRIFA028371a
PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).
1.0e-08:103:33
RATTUS NORVEGICUS (RAT).
Q01177

HRIFA028402a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
3.2e-33:204:39
THERMOMONOSPORA CURVATA.
P49695

HRIFA028440a
COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.
1.9e-07:192:36
HOMO SAPIENS (HUMAN).
P53420

HRIFA028468a
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN (EC 2.7.1.123) (CAM KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].
5.8e-32:178:44
RATTUS NORVEGICUS (RAT).
P13234

HRIFA028501a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).
6.3e-05:161:31
RATTUS NORVEGICUS (RAT).
P17659

HRIFA028511a
ANKYRIN HOMOLOG PRECURSOR.
3.0e-19:176:34
CHROMATIUM VINOSUM.
Q06527

HRIFA028576a
ACROSIN PRECURSOR (EC 3.4.21.10).
4.8e-08:78:46
ORYCTOLAGUS CUNICULUS (RABBIT).
P48038

HRIFA028614a
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
1.0e-08:82.39
PLASMODIUM LOPHURAE.
P04929

HRIFA028651a
BAND 3 ANION TRANSPORT PROTEIN.
1.3e-18:156:32
GALLUS GALLUS (CHICKEN).
P15575

HRIFA028790a
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
5.0e-18:212:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986

HRIFA028804a
CCAAT-BINDING FACTOR (CBF).
0.98:232:23
MUS MUSCULUS (MOUSE).
P53569

HRIFA028867a
REGULATORY PROTEIN E2.
0.0057:124:31
HUMAN PAPILLOMAVIRUS TYPE 25.
P36787

HRIFA028911a
HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.
1.2e-09:206:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47179

HRIFA028983a
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).
0.0051:115:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439

HRIFA029002a
FIBRINOGEN BETA CHAIN.
3.2e-25:121:45
BOS TAURUS (BOVINE).
P02676

HRIFA029050a
RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).
1.2e-10:134:32
GALLUS GALLUS (CHICKEN).

P24503

HRIFA029208a
RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).
1.4e-14:64:59
RATTUS NORVEGICUS (RAT).
Q02975

HRIFA029209a
"ALPHA-MANNOSIDASE II (EC 3.2.1.114) (MANNOSYL-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE) (MAN II) (GOLGI ALPHA-MANNOSIDASE II)."
2.3e-12:114:37
MUS MUSCULUS (MOUSE).
P27046

HRIFA029256a
GAP JUNCTION BETA-2 PROTEIN (CONNEXIN 26) (CX26).
1.8e-35:89:75
HOMO SAPIENS (HUMAN).
P29033

HRIFA029263a
SARCALUMENIN PRECURSOR.
2.1e-16:161:31
ORYCTOLAGUS CUNICULUS (RABBIT).
P13666

HRIFA029278a
"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6" PEPTIDE P-H].
3.5e-10:204:32
HOMO SAPIENS (HUMAN).
P04280

HRIFA029285a
GLYCOPROTEIN 25L PRECURSOR (GP25L).
4.9e-58:197:55
CANIS FAMILIARIS (DOG).
P27869

HRIFA029317a
HIGH AFFINITY SULPHATE TRANSPORTER 2.
2.3e-25:83:50
STYLOSANTHES HAMATA.
P53392

HRIFA029327a
MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN (OGCP).
9.1e-34:227:37
BOS TAURUS (BOVINE).
P22292

HRIFA029349a
CUTICLE COLLAGEN 12 PRECURSOR.
5.1e-09:190:33
CAENORHABDITIS ELEGANS.
P20630

HRIFA029393a
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
9.7e-69:165:84
HOMO SAPIENS (HUMAN).
P35414

HRIFA029398a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.011:170:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128

HRIFA029425a
ALPHA CRYSTALLIN B CHAIN (ALPHA(B)-CRYSTALLIN).
2.0e-08:99:32
BOS TAURUS (BOVINE).
P02510

HRIFA029434a
"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CPS) [CONTAINS: BASIC PEPTIDE IB-6" PEPTIDE P-H].
2.6e-05:232:32
HOMO SAPIENS (HUMAN).
P04280

HRIFA029440a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.00046:131:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA029460a
SYNAPTOTAGMIN III.
1.5e-08:102:35
RATTUS NORVEGICUS (RAT).
P40748

HRIFA029467a
GLYCOPROTEIN X PRECURSOR.
5.2e-07:182:31
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

HRIFA029508a
PROPERDIN PRECURSOR.
1.9e-06:218:32
HOMO SAPIENS (HUMAN).
P27918

HRIFA029511a
POTASSIUM CHANNEL PROTEIN EAG.
2.3e-66:139:61
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q02280

HRIFA029602a
SEX-DETERMINING REGION Y PROTEIN (TESTIS-DETERMINING FACTOR).
1.0:37:37

SUS SCROFA (PIG).
P36393

HRIFA029649a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
0.30:99:34
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284

HRIFA029715a
GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-DAMAGE INDUCIBLE TRANSCRIPT 3) (DDIT3) (C/EBP-HOMOLOGOUS PROTEIN) (CHOP).
0.54:95:30
HOMO SAPIENS (HUMAN).
P35638

HRIFA029730a
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
3.8e-05:131:29
PLASMODIUM LOPHURAE.
P04929

HRIFA029792a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
9.0e-09:178:30
THERMOMONOSPORA CURVATA.
P49695

HRIFA029802a
TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN).
7.2e-73:204:69
CANIS FAMILIARIS (DOG).
Q01685

HRIFA029866a
PROTEIN KINASE BYR2 (EC 2.7.1.-) (PROTEIN KINASE STE8) (MAPK KINASE KINASE) (MAPKKK).
1.2e-27:144:45
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P28829

HRIFA029932a
F-SPONDIN PRECURSOR.
9.1e-24:191:37
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P35447

HRIFA030025a
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
1.0e-11:138:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802

HRIFA030045a
SARCALUMENIN PRECURSOR.
2.4e-20:151:32
ORYCTOLAGUS CUNICULUS (RABBIT).
P13666

HRIFA030103a
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
2.1e-05:215:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53214

HRIFA030106a
SCO-SPONDIN (FRAGMENT).
0.53:60:36
BOS TAURUS (BOVINE).
P98167

HRIFA030147a
PUTATIVE MITOCHONDRIAL CARRIER YGR096W.
1.8e-10:93:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53257

HRIFA030250a
ENAMELIN (TUFTELIN).
3.7e-108:250:86
BOS TAURUS (BOVINE).
P27628

HRIFA030264a
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).
3.3e-09:119:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170

HRIFA030342a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).
1.5e-42:203:49
HOMO SAPIENS (HUMAN).
P37058

HRIFA030370a
HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.
8.0e-12:88:48
MYCOBACTERIUM TUBERCULOSIS.
Q10555

HRIFA030371a
"PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU)."
1.6e-68:228:59
HOMO SAPIENS (HUMAN).
Q15139

HRIFA030381a
COLLAGEN 1(X) CHAIN PRECURSOR.
3.0e-05:204:30
GALLUS GALLUS (CHICKEN).
P08125

HRIFA030385a
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.

0.029:162:31
HOMO SAPIENS (HUMAN).
Q03692

HRIFA030411a
SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).
1.2e-27:115:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09925

HRIFA030448a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
2.5e-92:225:77
HOMO SAPIENS (HUMAN).
P27448

HRIFA030456a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
9.3e-08:127:35
MUS MUSCULUS (MOUSE).
P05142

HRIFA030461a
CUTICLE COLLAGEN 12 PRECURSOR.
0.046:140:31
CAENORHABDITIS ELEGANS.
P20630

HRIFA030472a
NUC-1 NEGATIVE REGULATORY PROTEIN PREG.
0.0030:98:31
NEUROSPORA CRASSA.
Q06712

HRIFA030509a
"INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE (EC 2.7.1.-) (INTERFERON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE) (P68 KINASE) (P1/EIF-2A PROTEIN KINASE)."
2.5e-09:65:43
HOMO SAPIENS (HUMAN).
P19525

HRIFA030511a
T-LYMPHOCYTE MATURATION-ASSOCIATED PROTEIN.
0.00010:99:33
HOMO SAPIENS (HUMAN).
P21145

HRIFA030545a
PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).
7.6e-21:165:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53974

HRIFA030566a
"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."
2.7e-07:221:30

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640

HRIFA030599a
GLYCOPROTEIN X PRECURSOR.
2.8e-05:236:27
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

HRIFA030629a
PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55).
3.5e-16:115:38
BOS TAURUS (BOVINE).
P05307

HRIFA030642a
SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).
2.5e-12:93:47
VOLVOX CARTERI.
P21997

HRIFA030662a
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
9.1e-120:279:83
HOMO SAPIENS (HUMAN).
P03886

HRIFA030839a
HYPOTHETICAL GENE 51 MEMBRANE PROTEIN.
1.0:66:27
ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV).
Q00135

HRIFA031091a
PROTEIN Q300.
0.0042:27:62
MUS MUSCULUS (MOUSE).
Q02722

HRIFA031126a
P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (RB INTRON ENCODED G-PROTEIN COUPLED RECEPTOR).
1.3e-06:70:34
HOMO SAPIENS (HUMAN).
P43657

HRIFA031249a
ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).
5.9e-05:166:31
RATTUS NORVEGICUS (RAT).
P04474

HRIFA031336a
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).
6.6e-15:97:38
PETROMYZON MARINUS (SEA LAMPREY).

P25210

HRIFA031395a
COLD SHOCK PROTEIN CSPB (FRAGMENT).
0.95:32:40
BACILLUS GLOBISPORUS.
P41018

HRIFA031397a
REGULATORY PROTEIN E2.
0.0077:145:35
HUMAN PAPILLOMAVIRUS TYPE 47.
P22420

HRIFA031438a
GLUCOSE REPRESSION MEDIATOR PROTEIN.
1.3e-06:176:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14922

HRIFA031869a
TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY-LIKE) (RHL).
1.7e-18:163:41
RATTUS NORVEGICUS (RAT).
Q04666

HRIFA031935a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
1.8e-06:192:32
ZEA MAYS (MAIZE).
P14918

HRIFA031986a
SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21-ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2).
2.4e-49:222:47
RATTUS NORVEGICUS (RAT).
P35465

HRIFA032009a
PROBABLE G PROTEIN-COUPLED RECEPTOR FROM T-CELLS PRECURSOR (GLUCOCORTICOID-INDUCED RECEPTOR).
1.0e-17:118:36
MUS MUSCULUS (MOUSE).
P30731

HRIFA032011a
MUSCARINIC ACETYLCHOLINE RECEPTOR M4.
7.8e-35:184:32
HOMO SAPIENS (HUMAN).
P08173

HRIFA032070a
MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
2.1e-18:107:44
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23500

HRIFA032073a
SECRETOGRANIN III PRECURSOR (SGIII).
9.7e-69:182:76
MUS MUSCULUS (MOUSE).
P47867

HRIFA032079a
HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I.
3.5e-12:96:39
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09906

HRIFA032097a
GLYCOPROTEIN J.
0.023:61:32
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P06480

HRIFA032161a
CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (NUCLEAR FACTOR NF-IL6-BETA) (NF-IL6-BETA).
0.22:56:42
HOMO SAPIENS (HUMAN).
P49716

HRIFA032186a
D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN) (TAXREB302).
0.86:50:38
HOMO SAPIENS (HUMAN).
Q10586

HRIFA032224a
HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.
2.6e-43:196:45
CAENORHABDITIS ELEGANS.
Q03567

HRIFA032257a
GLUCOSE REPRESSION MEDIATOR PROTEIN.
4.7e-07:204:25
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14922

HRIFA032274a
ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).
7.8e-60:163:74
MUS MUSCULUS (MOUSE).
Q07231

HRIFA032275a
CELL DIVISION CONTROL PROTEIN 28 (EC 2.7.1.-).
7.2e-41:179:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P00546

HRIFA032360a
HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.
3.0e-05:198:28

CAENORHABDITIS ELEGANS.
Q09625

HRIFA032389a
EBNA-1 NUCLEAR PROTEIN.
1.3e-05:86:39
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). P03211

HRIFA032433a
GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).
3.1e-14:54:53
RATTUS NORVEGICUS (RAT).
P30969

HRIFA032453a
BUTYROPHILIN PRECURSOR (BT).
5.9e-13:162:32
BOS TAURUS (BOVINE).
P18892

HRIFA032478a
GLYCOPROTEIN X PRECURSOR.
3.8e-06:253:28
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

HRIFA032506a
COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR.
1.2e-06:226:34
HOMO SAPIENS (HUMAN).
P12111

HRIFA032511a
COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.
8.7e-09:229:34
HOMO SAPIENS (HUMAN).
Q07092

HRIFA032530a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
9.0e-05:159:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA032587a
SYNAPTOTAGMIN (P65).
3.2e-08:72:52
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
P41823

HRIFA032605a
ANTIGEN PEPTIDE TRANSPORTER 1 (APT1) (PEPTIDE TRANSPORTER TAP1) (PEPTIDE TRANSPORTER PSF1) (PEPTIDE SUPPLY FACTOR 1) (PSF-1) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESSING 1).
8.4e-37:192:41
HOMO SAPIENS (HUMAN).
Q03518

HRIFA032642a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.0e-05:127:33
MUS MUSCULUS (MOUSE).
P05142

HRIFA032696a
COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).
1.4e-13:200:38
BOS TAURUS (BOVINE).
P02459

HRIFA032730a
K-GLYPICAN PRECURSOR.
4.8e-67:180:68
MUS MUSCULUS (MOUSE).
P51655

HRIFA032820a
GLUTAMIC ACID-RICH PROTEIN PRECURSOR.
7.5e-05:192:23
PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).
P13816

Homology search result 2

[0290] Homology of representative sequences of the 5'-end cluster to the data in Swiss-Prot database

[0291] Representative sequence of the 5'-end cluster exhibiting relatively high homology (304 cluster: "exhibiting relatively high homology" means that the P value is 10^{-10} or less)

HRIFA000327a, HRIFA000432a, HRIFA000553a, HRIFA000564a, HRIFA000631a, HRIFA000683a, HRIFA000776a, HRIFA000814a, HRIFA001132a, HRIFA001138a, HRIFA001337a, HRIFA001341a, HRIFA001489a, HRIFA001712a, HRIFA001720a, HRIFA001942a, HRIFA001975a, HRIFA001984a, HRIFA002384a, HRIFA002503a, HRIFA002743a, HRIFA002766a, HRIFA002805a, HRIFA002891a, HRIFA002919a, HRIFA002980a, HRIFA003063a, HRIFA003093a, HRIFA003635a, HRIFA004006a, HRIFA004034a, HRIFA004112a, HRIFA004426a, HRIFA004490a, HRIFA004523a, HRIFA004663a, HRIFA004696a, HRIFA004714a, HRIFA004745a, HRIFA004919a, HRIFA005184a, HRIFA005231a, HRIFA005240a, HRIFA005271a, HRIFA005372a, HRIFA005392a, HRIFA005409a, HRIFA005420a, HRIFA005438a, HRIFA005462a, HRIFA005644a, HRIFA005720a, HRIFA005732a, HRIFA005760a, HRIFA005781a, HRIFA006183a, HRIFA006494a, HRIFA006510a, HRIFA006566a, HRIFA006586a, HRIFA006596a, HRIFA006649a, HRIFA006667a, HRIFA006730a, HRIFA006926a, HRIFA007013a, HRIFA007219a, HRIFA007228a, HRIFA007243a, HRIFA007352a, HRIFA007424a, HRIFA007435a, HRIFA007463a, HRIFA007493a, HRIFA007571a, HRIFA007659a, HRIFA007722a, HRIFA007745a, HRIFA008000a, HRIFA008200a, HRIFA008284a, HRIFA008314a, HRIFA008362a, HRIFA008459a, HRIFA008483a, HRIFA008547a, HRIFA008611a, HRIFA008661a, HRIFA008717a, HRIFA008784a, HRIFA008981a, HRIFA009101a, HRIFA009171a, HRIFA009220a, HRIFA009451a, HRIFA009482a, HRIFA009783a, HRIFA009881a, HRIFA010085a, HRIFA010090a,
HRIFA010130a, HRIFA010319a, HRIFA010394a, HRIFA010460a, HRIFA010790a, HRIFA010975a, HRIFA011016a, HRIFA011179a, HRIFA011197a, HRIFA011449a, HRIFA011659a, HRIFA011947a, HRIFA012278a, HRIFA012584a, HRIFA012625a, HRIFA012692a, HRIFA012795a, HRIFA012885a, HRIFA012914a, HRIFA012969a, HRIFA012990a, HRIFA013254a, HRIFA013265a, HRIFA013276a, HRIFA013376a, HRIFA013477a, HRIFA013586a, HRIFA013726a, HRIFA013744a, HRIFA013911a, HRIFA014006a, HRIFA014185a, HRIFA014336a, HRIFA014465a, HRIFA014500a, HRIFA014561a, HRIFA014568a, HRIFA014621a, HRIFA014688a, HRIFA014819a, HRIFA014951a, HRIFA014967a, HRIFA015063a, HRIFA015070a, HRIFA015246a, HRIFA015423a, HRIFA015453a, HRIFA015486a, HRIFA015506a, HRIFA015536a, HRIFA015547a, HRIFA015568a, HRIFA015756a, HRIFA015811a, HRIFA016070a, HRIFA016290a, HRIFA016430a, HRIFA016654a, HRIFA016758a, HRIFA017031a, HRIFA017257a, HRIFA017295a, HRIFA017312a, HRIFA017703a, HRIFA017855a, HRIFA018092a, HRIFA018131a, HRIFA018134a, HRIFA018580a, HRIFA018827a, HRIFA018904a, HRIFA018993a, HRIFA019105a, HRIFA019136a, HRIFA019175a, HRIFA019262a, HRIFA019466a, HRIFA019867a, HRIFA019869a, HRIFA020272a, HRIFA020335a, HRIFA020349a, HRIFA020862a, HRIFA021213a, HRIFA021398a, HRIFA021499a, HRIFA021637a, HRIFA021651a, HRIFA021754a, HRIFA021781a, HRIFA022065a, HRIFA022139a, HRIFA022166a, HRIFA022177a, HRIFA022182a, HRIFA022227a, HRIFA022249a, HRIFA022265a,

HRIFA022328a, HRIFA022423a, HRIFA022528a, HRIFA022546a, HRIFA022564a, HRIFA022616a, HRIFA022671a, HRIFA022691a, HRIFA022707a, HRIFA022729a, HRIFA022737a, HRIFA022776a, HRIFA022875a, HRAFA022895a, HRIFA023007a, HRIFA023227a, HRIFA023257a, HRIFA023304a, HRIFA023464a, HRIFA023767a, HRIFA023923a, HRIFA024132a, HRIFA024255a, HRIFA024392a, HRIFA024423a, HRIFA024504a, HRIFA024718a, HRIFA024767a, HRIFA024937a, HRIFA024994a, HRIFA025046a, HRIFA025250a, HRIFA025261a, HRIFA025353a, HRIFA025492a, HRIFA025636a, HRIFA025695a, HRIFA025706a, HRIFA025766a, HRIFA025800a, HRIFA025907a, HRIFA025913a, HRIFA026089a, HRIFA026364a, HRIFA026496a, HRIFA026789a, HRIFA026813a, HRIFA026860a, HRIFA027012a, HRIFA027045a, HRIFA027125a, HRIFA027179a, HRIFA027187a, HRIFA027622a, HRIFA027625a, HRIFA027656a, HRIFA027681a, HRIFA027722a, HRIFA027940a, HRIFA028157a, HRIFA028402a, HRIFA028468a, HRIFA028511a, HRIFA028651a, HRIFA028790a, HRIFA029002a, HRIFA029208a, HRIFA029209a, HRIFA029256a, HRIFA029263a, HRIFA029285a, HRIFA029317a, HRIFA029327a, HRIFA029393a, HRIFA029511a, HRIFA029802a, HRIFA029866a, HRIFA029932a, HRIFA030025a, HRIFA030045a, HRIFA030250a, HRIFA030342a, HRIFA030370a, HRIFA030371a, HRIFA030411a, HRIFA030448a, HRIFA030545a, HRIFA030629a, HRIFA030642a, HRIFA030662a, HRIFA031336a, HRIFA031869a, HRIFA031986a, HRIFA032009a, HRIFA032011a, HRIFA032070a, HRIFA032073a, HRIFA032079a, HRIFA032224a, HRIFA032274a, HRIFA032275a, HRIFA032433a,
HRIFA032453a, HRIFA032605a, HRIFA032696a, HRIFA032730a,

Homology search result 3

[0292] Representative sequence of the 5'-end cluster exhibiting relatively low homology (221 cluster: "exhibiting relatively low homology" means that the P value is higher than 10^{-10} and 10^{-4} or less)
HRIFA000016a, HRIFA000071a, HRIFA000116a, HRIFA000123a, HRIFA000264a, HRIFA000415a, HRIFA000446a, HRIFA000695a, HRIFA000845a, HRIFA001971a, HRIFA002063a, HRIFA002102a, HRIFA002284a, HRIFA002309a, HRIFA002694a, HRIFA002762a, HRIFA002787a, HRIFA003055a, HRIFA003340a, HRIFA003402a, HRIFA003504a, HRIFA003892a, HRIFA003946a, HRIFA004162a, HRIFA004401a, HRIFA004780a, HRIFA005072a, HRIFA005102a, HRIFA005214a, HRIFA005255a, HRIFA005300a, HRIFA005369a, HRIFA005702a, HRIFA005728a, HRIFA005944a, HRIFA006298a, HRIFA006448a, HRIFA006572a, HRIFA006633a, HRIFA006642a, HRIFA007068a, HRIFA007244a, HRIFA007262a, HRIFA007512a, HRIFA007532a, HRIFA007565a, HRIFA007728a, HRIFA007909a, HRIFA008174a, HRIFA008426a, HRIFA008596a, HRIFA008790a, HRIFA008989a, HRIFA009578a, HRIFA009825a, HRIFA009852a, HRIFA009983a, HRIFA010005a, HRIFA010078a, HRIFA010152a, HRIFA010301a, HRIFA010361a, HRIFA010425a, HRIFA010466a, HRIFA010799a, HRIFA011580a, HRIFA011820a, HRIFA012167a, HRIFA012354a, HRIFA012427a, HRIFA012436a, HRIFA012515a, HRIFA012702a, HRIFA012737a, HRIFA013135a, HRIFA013235a, HRIFA013279a, HRIFA013589a, HRIFA013620a, HRIFA013919a, HRIFA013932a, HRIFA014056a, HRIFA014111a, HRIFA014133a, HRIFA014396a, HRIFA014397a, HRIFA014598a, HRIFA014702a, HRIFA014868a, HRIFA015219a, HRIFA015995a, HRIFA016214a, HRIFA016240a, HRIFA016255a, HRIFA016639a, HRIFA016963a, HRIFA017457a, HRIFA017643a, HRIFA017670a,
HRIFA017801a, HRIFA017836a, HRIFA017921a, HRIFA018238a, HRIFA018262a, HRIFA018287a, HRIFA018666a, HRIFA018688a, HRIFA018754a, HRIFA018794a, HRIFA018870a, HRIFA018931a, HRIFA019412a, HRIFA019490a, HRIFA019498a, HRIFA019532a, HRIFA019651a, HRIFA020144O, HRIFA020184a, HRIFA020453a, HRIFA020693a, HRIFA020707a, HRIFA020748a, HRIFA021061a, HRIFA021224a, HRIFA021494a, HRIFA021794a, HRIFA021855a, HRIFA021906a, HRIFA022156a, HRIFA022203a, HRIFA022234a, HRIFA022702a, HRIFA022728a, HRIFA022782a, HRIFA022865a, HRIFA022890a, HRIFA022985a, HRIFA023048a, HRIFA023069a, HRIFA023129a, HRIFA023154a, HRIFA023212a, HRIFA023489a, HRIFA023634a, HRIFA023894a, HRIFA024088a, HRIFA024197a, HRIFA024218a, HRIFA024473a, HRIFA024482a, HRIFA024543a, HRIFA025327a, HRIFA025479a, HRIFA025488a, HRIFA025703a, HRIFA025771a, HRIFA025778a, HRIFA025904a, HRIFA025966a, HRIFA025978a, HRIFA026121a, HRIFA026242a, HRIFA026316a, HRIFA026382a, HRIFA026465a, HRIFA026519a, HRIFA026564a, HRIFA026576a, HRIFA026618a, HRIFA026659a, HRIFA026764a, HRIFA027327a, HRIFA027329a, HRIFA027355a, HRIFA027644a, HRIFA027673a, HRIFA027714a, HRIFA027860a, HRIFA028061a, HRIFA028187a, HRIFA028262a, HRIFA028371a, HRIFA028440a, HRIFA028501a, HRIFA028576a, HRIFA028614a, HRIFA028911a, HRIFA029050a, HRIFA029278a, HRIFA029349a, HRIFA029425a, HRIFA029434a, HRIFA029460a, HRIFA029467a, HRIFA029508a, HRIFA029730a, HRIFA029792a, HRIFA030103a, HRIFA030147a,
HRIFA030264a, HRIFA030381a, HRIFA030456a, HRIFA030509a, HRIFA030511a, HRIFA030566a, HRIFA030599a, HRIFA031126a, HRIFA031249a, HRIFA031438a, HRIFA031935a, HRIFA032257a, HRIFA032360a, HRIFA032389a, HRIFA032478a, HRIFA032506a, HRIFA032511a, HRIFA032530a, HRIFA032587a, HRIFA032642a, HRIFA032820a,

Homology search result 4

[0293] Representative sequence of the 5'-end cluster exhibiting low homology (115 cluster: "exhibiting low homology"

means that the P value is higher than 10^{-4} and 1 or less)
HRIFA001099a, HRIFA001200a, HRIFA001413a, HRIFA001439a, HRIFA001558a, HRIFA001866a, HRIFA001972a, HRIFA002689a, HRIFA003357a, HRIFA003592a, HRIFA003640a, HRIFA003883a, HRIFA005296a, HRIFA005500a, HRIFA005540a, HRIFA006250a, HRIFA006609a, HRIFA006798a, HRIFA007032a, HRIFA007152a, HRIFA007547a, HRIFA007829a, HRIFA007985a, HRIFA008212a, HRIFA008252a, HRIFA008976a, HRIFA009071a, HRIFA009123a, HRIFA009136a, HRIFA009339a, HRIFA009762a, HRIFA010176a, HRIFA010490a, HRIFA010736a, HRIFA010859a, HRIFA010891a, HRIFA010988a, HRIFA011105a, HRIFA011128a, HRIFA011484a, HRIFA011512a, HRIFA011926a, HRIFA012069a, HRIFA012151a, HRIFA013092a, HRIFA013103a, HRIFA013980a, HRIFA014024a, HRIFA014590a, HRIFA014620a, HRIFA015122a, HRIFA015351a, HRIFA015802a, HRIFA015902a, HRIFA015947a, HRIFA016599a, HRIFA017146a, HRIFA017190a, HRIFA017456a, HRIFA017791a, HRIFA017818a, HRIFA018447a, HRIFA019437a, HRIFA019958a, HRIFA020883a, HRIFA021007a, HRIFA021040a, HRIFA021445a, HRIFA021543a, HRIFA021620a, HRIFA021787a, HRIFA022055a, HRIFA022335a, HRIFA022348a, HRIFA022411a, HRIFA022462a, HRIFA022493a, HRIFA022714a, HRIFA023434a, HRIFA024185a, HRIFA024305a, HRIFA024884a, HRIFA024893a, HRIFA024978a, HRIFA025033a, HRIFA025290a, HRIFA026265a, HRIFA026303a, HRIFA026351a, HRIFA026615a, HRIFA026923a, HRIFA027173a, HRIFA027485a, HRIFA027536a, HRIFA027549a, HRIFA027867a, HRIFA028804a, HRIFA028867a, HRIFA028983a, HRIFA029398a,
HRIFA029440a, HRIFA029602a, HRIFA029649a, HRIFA029715a, HRIFA030106a, HRIFA030385a, HRIFA030461a, HRIFA030472a, HRIFA030839a, HRIFA031091a, HRIFA031395a, HRIFA031397a, HRIFA032097a, HRIFA032161a, HRIFA032186a.

Homology search result 5

[0294] The result of the homology search in the SwissProt using the clone sequences of the 5'-ends.

Indicated are from the top,
the name of the clone sequence,
definition of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the organism of which the top hit data is obtained,
the Accession No. of the top hit data.

[0295] Data were not shown for the clones in which the P-value was higher than 1.

F-BNGH41000020
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
1.2e-119:279:83
HOMO SAPIENS (HUMAN).
P03886

F-BNGH41000087
PROPERDIN PRECURSOR.
2.5e-06:218:32
HOMO SAPIENS (HUMAN).
P27918

F-BNGH41000091
POTASSIUM CHANNEL PROTEIN EAG.
3.1e-66:139:61
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q02280

F-HEMBA1000006
S-ANTIGEN PROTEIN PRECURSOR.
3.0e-05:164:31
PLASMODIUM FALCIPARUM (ISOLATE V1).
P09593

F-HEMBA1000121

Homo sapiens DNA recombination and repair protein (MRE11B) mRNA, complete cds
0.00075:456:59
Hs.153855:AF022778

R-Y79AA1002213
Human mRNA for KIAA0392 gene, partial cds
6.2e-45:304:85
Hs.40100:AB002390

R-Y79AA1002334
ESTs
7.7e-91:495:92
Hs.90804:W28091

R-Y79AA1002373
Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end
5.2e-98:545:91
Hs.103948:K00627

R-Y79AA1002376
ESTs
2.0e-91:455:97
Hs.153375:AI287812

R-Y79AA1002378
ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-35 [Mus musculus]
9.4e-15:131:83
Hs.20082:W89121

R-Y79AA1002381
ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1/thailand)]
1.5e-104:531:95
Hs.26322:AA156858

Homology search result 10

[0305] Data obtained by the homology search for full length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.

C-HEMBA1000006//Homo sapiens mRNA; cDNA DKFZp564G1762 (from clone DKFZp564G1762).//0//1230bp//92%//AB026894
C-nnnnnnnnnnnn//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//2.30E-71//344aa//50%//P50636
C-HEMBA1000121//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//4.80E-05//83aa//27%//P34679
C-HEMBA1000128//PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).//3.20E-07//89aa//34%//P33154
C-HEMBA1000275
C-HEMBA1000300
C-HEMBA1000349//ATP-BINDING CASSETTE TRANSPORTER 1.//5.30E-65//352aa//39%//P41233
C-HEMBA1000443//Homo sapiens CGI-96 protein mRNA, complete cds.//4.70E-129//686bp//91%//AF151854
C-HEMBA1000590//Homo sapiens mRNA for matrilin-4, partial.//2.00E-273//1254bp//99%//AJ007581
C-HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.//0//994bp//99%//AF116272
C-HEMBA1000713//Homo sapiens 10kD protein (BC10) mRNA, complete cds.//0//1254bp//99%//AF053470

NASE I).//1.00E-77//359aa//44%//Q14012
C-Y79AA1001013
C-Y79AA1001056//Homo sapiens MAID protein mRNA, complete cds.//0//1475bp//99%//AF113535
C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//8.90E-12//132aa//38%//Q13829
C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) (NF-KAPPA-B1 P84 /NF-KAPPA-B1 P98) [CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT] (FRAGMENT).//4.50E-09//144aa//31%//Q63369
C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds.//6.30E-306//1388bp//99%//AF038961
C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.//5.10E-106//351aa//58%//Q10005
C-Y79AA1001272//Homo sapiens retinoic acid repressible protein (RARG-1) mRNA, complete cds.//1.50E-183//867bp//98%//AF172066
C-Y79AA1001328//Mus musculus mRNA for Dll3 protein, complete cds.//1.90E-263//1988bp//79%//AB013440
C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//6.20E-66//609aa//31%//P48751
C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds.//0//1588bp//99%//AF169481
C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds.//0//2943bp//99%//AB007938
C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds.//0//2263bp//99%//AF119042
C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members.//0//1920bp//98%//X00734
C-Y79AA1001592
C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR.//1.10E-13//286aa//27%//Q99795
C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//Q12697
C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.//3.70E-126//532bp//78%//D87325
C-Y79AA1001795//Homo sapiens mRNA for GalT4 protein.//2.30E-250//1137bp//99%//Y15061
C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//3.40E-54//182aa//39%//P23500
C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds.//0//1871bp//99%//AF078851
C-Y79AA1001863
C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//2.20E-06//140aa//26%//P32507
C-Y79AA1002058//Mus musculus Gng3lg mRNA, complete cds.//4.10E-167//1145bp//83%//AF069954
C-Y79AA1002121//HISTONE H1.//4.90E-12//114aa//35%//P35060
C-Y79AA1002129
C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.//1.20E-98//262aa//41%//Q03567
C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%//P14922
C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds.//7.20E-147//680bp//79%//D87325
C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.//1.50E-304//1667bp//90%//U39045
C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds.//0//963bp//99%//AF155100
C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds.//0//1791bp//98%//AF035013

Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.

2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-829 and 2545, wherein said oligonucleotide comprises at least 15 nucleotides.

3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide com-

prising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence,3'-end nucleotide sequence is selected from the group consisting of:

SEQ ID NO:4 and SEQ ID NO:830
SEQ ID NO:5 and SEQ ID NO:831
SEQ ID NO:6 and SEQ ID NO:832
SEQ ID NO:7 and SEQ ID NO:833
SEQ ID NO:8 and SEQ ID NO:834
SEQ ID NO:9 and SEQ ID NO:835
SEQ ID NO:11 and SEQ ID NO:836
SEQ ID NO:12 and SEQ ID NO:837
SEQ ID NO:13 and SEQ ID NO:838
SEQ ID NO:14 and SEQ ID NO:839
SEQ ID NO:15 and SEQ ID NO:840
SEQ ID NO:16 and SEQ ID NO:841
SEQ ID NO:17 and SEQ ID NO:842
SEQ ID NO:18 and SEQ ID NO:843
SEQ ID NO:20 and SEQ ID NO:844
SEQ ID NO:22 and SEQ ID NO:845
SEQ ID NO:23 and SEQ ID NO:846
SEQ ID NO:24 and SEQ ID NO:847
SEQ ID NO:25 and SEQ ID NO:848
SEQ ID NO:26 and SEQ ID NO:849
SEQ ID NO:27 and SEQ ID NO:850
SEQ ID NO:28 and SEQ ID NO:851
SEQ ID NO:29 and SEQ ID NO:852
SEQ ID NO:30 and SEQ ID NO:853
SEQ ID NO:31 and SEQ ID NO:854
SEQ ID NO:32 and SEQ ID NO:855
SEQ ID NO:33 and SEQ ID NO:856
SEQ ID NO:34 and SEQ ID NO:857
SEQ ID NO:35 and SEQ ID NO:858
SEQ ID NO:36 and SEQ ID NO:859
SEQ ID NO:37 and SEQ ID NO:860
SEQ ID NO:39 and SEQ ID NO:861
SEQ ID NO:40 and SEQ ID NO:862
SEQ ID NO:41 and SEQ ID NO:863
SEQ ID NO:42 and SEQ ID NO:864
SEQ ID NO:44 and SEQ ID NO:865
SEQ ID NO:45 and SEQ ID NO:866
SEQ ID NO:46 and SEQ ID NO:867
SEQ ID NO:47 and SEQ ID NO:868

SEQ ID NO:48 and SEQ ID NO:869
SEQ ID NO:49 and SEQ ID NO:870
SEQ ID NO:50 and SEQ ID NO:871
SEQ ID NO:52 and SEQ ID NO:872
SEQ ID NO:53 and SEQ ID NO:873
SEQ ID NO:54 and SEQ ID NO:874
SEQ ID NO:55 and SEQ ID NO:875
SEQ ID NO:56 and SEQ ID NO:876
SEQ ID NO:57 and SEQ ID NO:877
SEQ ID NO:58 and SEQ ID NO:878
SEQ ID NO:59 and SEQ ID NO:879
SEQ ID NO:60 and SEQ ID NO:880
SEQ ID NO:61 and SEQ ID NO:881
SEQ ID NO:62 and SEQ ID NO:882
SEQ ID NO:63 and SEQ ID NO:883
SEQ ID NO:64 and SEQ ID NO:884
SEQ ID NO:65 and SEQ ID NO:885
SEQ ID NO:66 and SEQ ID NO:886
SEQ ID NO:67 and SEQ ID NO:887
SEQ ID NO:69 and SEQ ID NO:888
SEQ ID NO:70 and SEQ ID NO:889
SEQ ID NO:71 and SEQ ID NO:890
SEQ ID NO:72 and SEQ ID NO:891
SEQ ID NO:73 and SEQ ID NO:892
SEQ ID NO:74 and SEQ ID NO:893
SEQ ID NO:75 and SEQ ID NO:894
SEQ ID NO:76 and SEQ ID NO:895
SEQ ID NO:77 and SEQ ID NO:896
SEQ ID NO:78 and SEQ ID NO:897
SEQ ID NO:79 and SEQ ID NO:898
SEQ ID NO:80 and SEQ ID NO:899
SEQ ID NO:81 and SEQ ID NO:900
SEQ ID NO:82 and SEQ ID NO:901
SEQ ID NO:83 and SEQ ID NO:902
SEQ ID NO:84 and SEQ ID NO:903
SEQ ID NO:85 and SEQ ID NO:904
SEQ ID NO:86 and SEQ ID NO:905
SEQ ID NO:87 and SEQ ID NO:906
SEQ ID NO:88 and SEQ ID NO:907
SEQ ID NO:89 and SEQ ID NO:908
SEQ ID NO:90 and SEQ ID NO:909
SEQ ID NO:91 and SEQ ID NO:910
SEQ ID NO:92 and SEQ ID NO:911
SEQ ID NO:93 and SEQ ID NO:912
SEQ ID NO:94 and SEQ ID NO:913
SEQ ID NO:95 and SEQ ID NO:914
SEQ ID NO:96 and SEQ ID NO:915
SEQ ID NO:97 and SEQ ID NO:916
SEQ ID NO:98 and SEQ ID NO:917
SEQ ID NO:99 and SEQ ID NO:918
SEQ ID NO:100 and SEQ ID NO:919
SEQ ID NO:101 and SEQ ID NO:920

SEQ ID NO:102 and SEQ ID NO:921
SEQ ID NO:103 and SEQ ID NO:922
SEQ ID NO:104 and SEQ ID NO:923
SEQ ID NO:105 and SEQ ID NO:924
SEQ ID NO:106 and SEQ ID NO:925
SEQ ID NO:107 and SEQ ID NO:926
SEQ ID NO:108 and SEQ ID NO:927
SEQ ID NO:109 and SEQ ID NO:928
SEQ ID NO:110 and SEQ ID NO:929
SEQ ID NO:111 and SEQ ID NO:930
SEQ ID NO:112 and SEQ ID NO:931
SEQ ID NO:113 and SEQ ID NO:932
SEQ ID NO:114 and SEQ ID NO:933
SEQ ID NO:115 and SEQ ID NO:934
SEQ ID NO:116 and SEQ ID NO:935
SEQ ID NO:117 and SEQ ID NO:936
SEQ ID NO:118 and SEQ ID NO:937
SEQ ID NO:119 and SEQ ID NO:938
SEQ ID NO:120 and SEQ ID NO:939
SEQ ID NO:122 and SEQ ID NO:940
SEQ ID NO:123 and SEQ ID NO:941
SEQ ID NO:124 and SEQ ID NO:942
SEQ ID NO:125 and SEQ ID NO:943
SEQ ID NO:126 and SEQ ID NO:944
SEQ ID NO:127 and SEQ ID NO:945
SEQ ID NO:128 and SEQ ID NO:946
SEQ ID NO:129 and SEQ ID NO:947
SEQ ID NO:130 and SEQ ID NO:948
SEQ ID NO:131 and SEQ ID NO:949
SEQ ID NO:132 and SEQ ID NO:950
SEQ ID NO:133 and SEQ ID NO:951
SEQ ID NO:134 and SEQ ID NO:952
SEQ ID NO:135 and SEQ ID NO:953
SEQ ID NO:136 and SEQ ID NO:954
SEQ ID NO:137 and SEQ ID NO:955
SEQ ID NO:138 and SEQ ID NO:956
SEQ ID NO:139 and SEQ ID NO:957
SEQ ID NO:140 and SEQ ID NO:958
SEQ ID NO:141 and SEQ ID NO:959
SEQ ID NO:142 and SEQ ID NO:960
SEQ ID NO:143 and SEQ ID NO:961
SEQ ID NO:144 and SEQ ID NO:962
SEQ ID NO:145 and SEQ ID NO:963
SEQ ID NO:146 and SEQ ID NO:964
SEQ ID NO:147 and SEQ ID NO:965
SEQ ID NO:148 and SEQ ID NO:966
SEQ ID NO:149 and SEQ ID NO:967
SEQ ID NO:150 and SEQ ID NO:968
SEQ ID NO:151 and SEQ ID NO:969
SEQ ID NO:152 and SEQ ID NO:970
SEQ ID NO:153 and SEQ ID NO:971
SEQ ID NO:154 and SEQ ID NO:972

SEQ ID NO:155 and SEQ ID NO:973
SEQ ID NO:156 and SEQ ID NO:974
SEQ ID NO:157 and SEQ ID NO:975
SEQ ID NO:158 and SEQ ID NO:976
SEQ ID NO:159 and SEQ ID NO:977
SEQ ID NO:160 and SEQ ID NO:978
SEQ ID NO:161 and SEQ ID NO:979
SEQ ID NO:162 and SEQ ID NO:980
SEQ ID NO:163 and SEQ ID NO:981
SEQ ID NO:164 and SEQ ID NO:982
SEQ ID NO:165 and SEQ ID NO:983
SEQ ID NO:166 and SEQ ID NO:984
SEQ ID NO:167 and SEQ ID NO:985
SEQ ID NO:168 and SEQ ID NO:986
SEQ ID NO:169 and SEQ ID NO:987
SEQ ID NO:170 and SEQ ID NO:988
SEQ ID NO:171 and SEQ ID NO:989
SEQ ID NO:172 and SEQ ID NO:990
SEQ ID NO:173 and SEQ ID NO:991
SEQ ID NO:174 and SEQ ID NO:992
SEQ ID NO:175 and SEQ ID NO:993
SEQ ID NO:176 and SEQ ID NO:994
SEQ ID NO:177 and SEQ ID NO:995
SEQ ID NO:178 and SEQ ID NO:996
SEQ ID NO:179 and SEQ ID NO:997
SEQ ID NO:180 and SEQ ID NO:998
SEQ ID NO:181 and SEQ ID NO:999
SEQ ID NO:182 and SEQ ID NO:1000
SEQ ID NO:183 and SEQ ID NO:1001
SEQ ID NO:184 and SEQ ID NO:1002
SEQ ID NO:185 and SEQ ID NO:1003
SEQ ID NO:186 and SEQ ID NO:1004
SEQ ID NO:187 and SEQ ID NO:1005
SEQ ID NO:188 and SEQ ID NO:1006
SEQ ID NO:189 and SEQ ID NO:1007
SEQ ID NO:190 and SEQ ID NO:1008
SEQ ID NO:191 and SEQ ID NO:1009
SEQ ID NO:193 and SEQ ID NO:1010
SEQ ID NO:194 and SEQ ID NO:1011
SEQ ID NO:195 and SEQ ID NO:1012
SEQ ID NO:196 and SEQ ID NO:1013
SEQ ID NO:197 and SEQ ID NO:1014
SEQ ID NO:198 and SEQ ID NO:1015
SEQ ID NO:199 and SEQ ID NO:1016
SEQ ID NO:200 and SEQ ID NO:1017
SEQ ID NO:201 and SEQ ID NO:1018
SEQ ID NO:202 and SEQ ID NO:1019
SEQ ID NO:203 and SEQ ID NO:1020
SEQ ID NO:204 and SEQ ID NO:1021
SEQ ID NO:205 and SEQ ID NO:1022
SEQ ID NO:207 and SEQ ID NO:1023
SEQ ID NO:208 and SEQ ID NO:1024

SEQ ID NO:209 and SEQ ID NO:1025
SEQ ID NO:210 and SEQ ID NO:1026
SEQ ID NO:211 and SEQ ID NO:1027
SEQ ID NO:212 and SEQ ID NO:1028
SEQ ID NO:213 and SEQ ID NO:1029
SEQ ID NO:214 and SEQ ID NO:1030
SEQ ID NO:215 and SEQ ID NO:1031
SEQ ID NO:216 and SEQ ID NO:1032
SEQ ID NO:248 and SEQ ID NO:1033
SEQ ID NO:249 and SEQ ID NO:1034
SEQ ID NO:250 and SEQ ID NO:1035
SEQ ID NO:251 and SEQ ID NO:1036
SEQ ID NO:252 and SEQ ID NO:1037
SEQ ID NO:253 and SEQ ID NO:1038
SEQ ID NO:254 and SEQ ID NO:1039
SEQ ID NO:255 and SEQ ID NO:1040
SEQ ID NO:256 and SEQ ID NO:1041
SEQ ID NO:257 and SEQ ID NO:1042
SEQ ID NO:258 and SEQ ID NO:1043
SEQ ID NO:259 and SEQ ID NO:1044
SEQ ID NO:260 and SEQ ID NO:1045
SEQ ID NO:261 and SEQ ID NO:1046
SEQ ID NO:262 and SEQ ID NO:1047
SEQ ID NO:263 and SEQ ID NO:1048
SEQ ID NO:264 and SEQ ID NO:1049
SEQ ID NO:265 and SEQ ID NO:1050
SEQ ID NO:266 and SEQ ID NO:1051
SEQ ID NO:267 and SEQ ID NO:1052
SEQ ID NO:268 and SEQ ID NO:1053
SEQ ID NO:291 and SEQ ID NO:1054
SEQ ID NO:292 and SEQ ID NO:1055
SEQ ID NO:293 and SEQ ID NO:1056
SEQ ID NO:294 and SEQ ID NO:1057
SEQ ID NO:295 and SEQ ID NO:1058
SEQ ID NO:296 and SEQ ID NO:1059
SEQ ID NO:297 and SEQ ID NO:1060
SEQ ID NO:298 and SEQ ID NO:1061
SEQ ID NO:300 and SEQ ID NO:1062
SEQ ID NO:301 and SEQ ID NO:1063
SEQ ID NO:302 and SEQ ID NO:1064
SEQ ID NO:304 and SEQ ID NO:1065
SEQ ID NO:305 and SEQ ID NO:1066
SEQ ID NO:306 and SEQ ID NO:1067
SEQ ID NO:307 and SEQ ID NO:1068
SEQ ID NO:308 and SEQ ID NO:1069
SEQ ID NO:309 and SEQ ID NO:1070
SEQ ID NO:310 and SEQ ID NO:1071
SEQ ID NO:311 and SEQ ID NO:1072
SEQ ID NO:312 and SEQ ID NO:1073
SEQ ID NO:313 and SEQ ID NO:1074
SEQ ID NO:314 and SEQ ID NO:1075
SEQ ID NO:315 and SEQ ID NO:1076

SEQ ID NO:317 and SEQ ID NO:1077
SEQ ID NO:318 and SEQ ID NO:1078
SEQ ID NO:319 and SEQ ID NO:1079
SEQ ID NO:320 and SEQ ID NO:1080
SEQ ID NO:321 and SEQ ID NO:1081
SEQ ID NO:322 and SEQ ID NO:1082
SEQ ID NO:323 and SEQ ID NO:1083
SEQ ID NO:324 and SEQ ID NO:1084
SEQ ID NO:325 and SEQ ID NO:1085
SEQ ID NO:326 and SEQ ID NO:1086
SEQ ID NO:327 and SEQ ID NO:1087
SEQ ID NO:328 and SEQ ID NO:1088
SEQ ID NO:329 and SEQ ID NO:1089
SEQ ID NO:330 and SEQ ID NO:1090
SEQ ID NO:331 and SEQ ID NO:1091
SEQ ID NO:332 and SEQ ID NO:1092
SEQ ID NO:333 and SEQ ID NO:1093
SEQ ID NO:334 and SEQ ID NO:1094
SEQ ID NO:335 and SEQ ID NO:1095
SEQ ID NO:336 and SEQ ID NO:1096
SEQ ID NO:337 and SEQ ID NO:1097
SEQ ID NO:338 and SEQ ID NO:1098
SEQ ID NO:339 and SEQ ID NO:1099
SEQ ID NO:340 and SEQ ID NO:1100
SEQ ID NO:341 and SEQ ID NO:1101
SEQ ID NO:342 and SEQ ID NO:1102
SEQ ID NO:343 and SEQ ID NO:1103
SEQ ID NO:344 and SEQ ID NO:1104
SEQ ID NO:345 and SEQ ID NO:1105
SEQ ID NO:347 and SEQ ID NO:1106
SEQ ID NO:348 and SEQ ID NO:1107
SEQ ID NO:349 and SEQ ID NO:1108
SEQ ID NO:350 and SEQ ID NO:1109
SEQ ID NO:351 and SEQ ID NO:1110
SEQ ID NO:352 and SEQ ID NO:1111
SEQ ID NO:353 and SEQ ID NO:1112
SEQ ID NO:354 and SEQ ID NO:1113
SEQ ID NO:355 and SEQ ID NO:1114
SEQ ID NO:356 and SEQ ID NO:1115
SEQ ID NO:357 and SEQ ID NO:1116
SEQ ID NO:358 and SEQ ID NO:1117
SEQ ID NO:359 and SEQ ID NO:1118
SEQ ID NO:360 and SEQ ID NO:1119
SEQ ID NO:361 and SEQ ID NO:1120
SEQ ID NO:362 and SEQ ID NO:1121
SEQ ID NO:363 and SEQ ID NO:1122
SEQ ID NO:364 and SEQ ID NO:1123
SEQ ID NO:365 and SEQ ID NO:1124
SEQ ID NO:366 and SEQ ID NO:1125
SEQ ID NO:367 and SEQ ID NO:1126
SEQ ID NO:368 and SEQ ID NO:1127
SEQ ID NO:369 and SEQ ID NO:1128

SEQ ID NO:370 and SEQ ID NO:1129
SEQ ID NO:371 and SEQ ID NO:1130
SEQ ID NO:372 and SEQ ID NO:1131
SEQ ID NO:373 and SEQ ID NO:1132
SEQ ID NO:374 and SEQ ID NO:1133
SEQ ID NO:375 and SEQ ID NO:1134
SEQ ID NO:376 and SEQ ID NO:1135
SEQ ID NO:377 and SEQ ID NO:1136
SEQ ID NO:378 and SEQ ID NO:1137
SEQ ID NO:379 and SEQ ID NO:1138
SEQ ID NO:380 and SEQ ID NO:1139
SEQ ID NO:381 and SEQ ID NO:1140
SEQ ID NO:382 and SEQ ID NO:1141
SEQ ID NO:383 and SEQ ID NO:1142
SEQ ID NO:384 and SEQ ID NO:1143
SEQ ID NO:385 and SEQ ID NO:1144
SEQ ID NO:386 and SEQ ID NO:1145
SEQ ID NO:387 and SEQ ID NO:1146
SEQ ID NO:388 and SEQ ID NO:1147
SEQ ID NO:389 and SEQ ID NO:1148
SEQ ID NO:390 and SEQ ID NO:1149
SEQ ID NO:391 and SEQ ID NO:1150
SEQ ID NO:392 and SEQ ID NO:1151
SEQ ID NO:393 and SEQ ID NO:1152
SEQ ID NO:394 and SEQ ID NO:1153
SEQ ID NO:395 and SEQ ID NO:1154
SEQ ID NO:396 and SEQ ID NO:1155
SEQ ID NO:397 and SEQ ID NO:1156
SEQ ID NO:398 and SEQ ID NO:1157
SEQ ID NO:399 and SEQ ID NO:1158
SEQ ID NO:400 and SEQ ID NO:1159
SEQ ID NO:401 and SEQ ID NO:1160
SEQ ID NO:402 and SEQ ID NO:1161
SEQ ID NO:403 and SEQ ID NO:1162
SEQ ID NO:404 and SEQ ID NO:1163
SEQ ID NO:405 and SEQ ID NO:1164
SEQ ID NO:406 and SEQ ID NO:1165
SEQ ID NO:407 and SEQ ID NO:1166
SEQ ID NO:408 and SEQ ID NO:1167
SEQ ID NO:409 and SEQ ID NO:1168
SEQ ID NO:410 and SEQ ID NO:1169
SEQ ID NO:411 and SEQ ID NO:1170
SEQ ID NO:412 and SEQ ID NO:1171
SEQ ID NO:413 and SEQ ID NO:1172
SEQ ID NO:414 and SEQ ID NO:1173
SEQ ID NO:415 and SEQ ID NO:1174
SEQ ID NO:416 and SEQ ID NO:1175
SEQ ID NO:417 and SEQ ID NO:1176
SEQ ID NO:419 and SEQ ID NO:1177
SEQ ID NO:420 and SEQ ID NO:1178
SEQ ID NO:421 and SEQ ID NO:1179
SEQ ID NO:422 and SEQ ID NO:1180

SEQ ID NO:423 and SEQ ID NO:1181
SEQ ID NO:424 and SEQ ID NO:1182
SEQ ID NO:425 and SEQ ID NO:1183
SEQ ID NO:426 and SEQ ID NO:1184
SEQ ID NO:427 and SEQ ID NO:1185
SEQ ID NO:428 and SEQ ID NO:1186
SEQ ID NO:429 and SEQ ID NO:1187
SEQ ID NO:430 and SEQ ID NO:1188
SEQ ID NO:431 and SEQ ID NO:1189
SEQ ID NO:432 and SEQ ID NO:1190
SEQ ID NO:433 and SEQ ID NO:1191
SEQ ID NO:434 and SEQ ID NO:1192
SEQ ID NO:435 and SEQ ID NO:1193
SEQ ID NO:436 and SEQ ID NO:1194
SEQ ID NO:437 and SEQ ID NO:1195
SEQ ID NO:438 and SEQ ID NO:1196
SEQ ID NO:439 and SEQ ID NO:1197
SEQ ID NO:440 and SEQ ID NO:1198
SEQ ID NO:441 and SEQ ID NO:1199
SEQ ID NO:442 and SEQ ID NO:1200
SEQ ID NO:443 and SEQ ID NO:1201
SEQ ID NO:444 and SEQ ID NO:1202
SEQ ID NO:446 and SEQ ID NO:1203
SEQ ID NO:447 and SEQ ID NO:1204
SEQ ID NO:448 and SEQ ID NO:1205
SEQ ID NO:450 and SEQ ID NO:1206
SEQ ID NO:451 and SEQ ID NO:1207
SEQ ID NO:452 and SEQ ID NO:1208
SEQ ID NO:453 and SEQ ID NO:1209
SEQ ID NO:454 and SEQ ID NO:1210
SEQ ID NO:455 and SEQ ID NO:1211
SEQ ID NO:456 and SEQ ID NO:1212
SEQ ID NO:457 and SEQ ID NO:1213
SEQ ID NO:458 and SEQ ID NO:1214
SEQ ID NO:459 and SEQ ID NO:1215
SEQ ID NO:460 and SEQ ID NO:1216
SEQ ID NO:461 and SEQ ID NO:1217
SEQ ID NO:462 and SEQ ID NO:1218
SEQ ID NO:463 and SEQ ID NO:1219
SEQ ID NO:464 and SEQ ID NO:1220
SEQ ID NO:465 and SEQ ID NO:1221
SEQ ID NO:466 and SEQ ID NO:1222
SEQ ID NO:467 and SEQ ID NO:1223
SEQ ID NO:468 and SEQ ID NO:1224
SEQ ID NO:469 and SEQ ID NO:1225
SEQ ID NO:470 and SEQ ID NO:1226
SEQ ID NO:471 and SEQ ID NO:1227
SEQ ID NO:472 and SEQ ID NO:1228
SEQ ID NO:473 and SEQ ID NO:1229
SEQ ID NO:474 and SEQ ID NO:1230
SEQ ID NO:475 and SEQ ID NO:1231
SEQ ID NO:476 and SEQ ID NO:1232

SEQ ID NO:477 and SEQ ID NO:1233
SEQ ID NO:478 and SEQ ID NO:1234
SEQ ID NO:479 and SEQ ID NO:1235
SEQ ID NO:480 and SEQ ID NO:1236
SEQ ID NO:481 and SEQ ID NO:1237
SEQ ID NO:482 and SEQ ID NO:1238
SEQ ID NO:483 and SEQ ID NO:1239
SEQ ID NO:484 and SEQ ID NO:1240
SEQ ID NO:485 and SEQ ID NO:1241
SEQ ID NO:486 and SEQ ID NO:1242
SEQ ID NO:487 and SEQ ID NO:1243
SEQ ID NO:488 and SEQ ID NO:1244
SEQ ID NO:489 and SEQ ID NO:1245
SEQ ID NO:490 and SEQ ID NO:1246
SEQ ID NO:492 and SEQ ID NO:1247
SEQ ID NO:493 and SEQ ID NO:1248
SEQ ID NO:494 and SEQ ID NO:1249
SEQ ID NO:496 and SEQ ID NO:1250
SEQ ID NO:497 and SEQ ID NO:1251
SEQ ID NO:498 and SEQ ID NO:1252
SEQ ID NO:499 and SEQ ID NO:1253
SEQ ID NO:500 and SEQ ID NO:1254
SEQ ID NO:501 and SEQ ID NO:1255
SEQ ID NO:502 and SEQ ID NO:1256
SEQ ID NO:503 and SEQ ID NO:1257
SEQ ID NO:504 and SEQ ID NO:1258
SEQ ID NO:505 and SEQ ID NO:1259
SEQ ID NO:506 and SEQ ID NO:1260
SEQ ID NO:507 and SEQ ID NO:1261
SEQ ID NO:508 and SEQ ID NO:1262
SEQ ID NO:509 and SEQ ID NO:1263
SEQ ID NO:510 and SEQ ID NO:1264
SEQ ID NO:511 and SEQ ID NO:1265
SEQ ID NO:513 and SEQ ID NO:1266
SEQ ID NO:514 and SEQ ID NO:1267
SEQ ID NO:515 and SEQ ID NO:1268
SEQ ID NO:516 and SEQ ID NO:1269
SEQ ID NO:517 and SEQ ID NO:1270
SEQ ID NO:518 and SEQ ID NO:1271
SEQ ID NO:519 and SEQ ID NO:1272
SEQ ID NO:520 and SEQ ID NO:1273
SEQ ID NO:521 and SEQ ID NO:1274
SEQ ID NO:522 and SEQ ID NO:1275
SEQ ID NO:523 and SEQ ID NO:1276
SEQ ID NO:524 and SEQ ID NO:1277
SEQ ID NO:525 and SEQ ID NO:1278
SEQ ID NO:526 and SEQ ID NO:1279
SEQ ID NO:527 and SEQ ID NO:1280
SEQ ID NO:528 and SEQ ID NO:1281
SEQ ID NO:529 and SEQ ID NO:1282
SEQ ID NO:530 and SEQ ID NO:1283
SEQ ID NO:531 and SEQ ID NO:1284

SEQ ID NO:532 and SEQ ID NO:1285
SEQ ID NO:533 and SEQ ID NO:1286
SEQ ID NO:534 and SEQ ID NO:1287
SEQ ID NO:535 and SEQ ID NO:1288
SEQ ID NO:536 and SEQ ID NO:1289
SEQ ID NO:537 and SEQ ID NO:1290
SEQ ID NO:538 and SEQ ID NO:1291
SEQ ID NO:539 and SEQ ID NO:1292
SEQ ID NO:540 and SEQ ID NO:1293
SEQ ID NO:541 and SEQ ID NO:1294
SEQ ID NO:542 and SEQ ID NO:1295
SEQ ID NO:543 and SEQ ID NO:1296
SEQ ID NO:544 and SEQ ID NO:1297
SEQ ID NO:545 and SEQ ID NO:1298
SEQ ID NO:546 and SEQ ID NO:1299
SEQ ID NO:547 and SEQ ID NO:1300
SEQ ID NO:548 and SEQ ID NO:1301
SEQ ID NO:549 and SEQ ID NO:1302
SEQ ID NO:550 and SEQ ID NO:1303
SEQ ID NO:551 and SEQ ID NO:1304
SEQ ID NO:552 and SEQ ID NO:1305
SEQ ID NO:553 and SEQ ID NO:1306
SEQ ID NO:554 and SEQ ID NO:1307
SEQ ID NO:555 and SEQ ID NO:1308
SEQ ID NO:556 and SEQ ID NO:1309
SEQ ID NO:557 and SEQ ID NO:1310
SEQ ID NO:558 and SEQ ID NO:1311
SEQ ID NO:559 and SEQ ID NO:1312
SEQ ID NO:560 and SEQ ID NO:1313
SEQ ID NO:561 and SEQ ID NO:1314
SEQ ID NO:562 and SEQ ID NO:1315
SEQ ID NO:563 and SEQ ID NO:1316
SEQ ID NO:564 and SEQ ID NO:1317
SEQ ID NO:565 and SEQ ID NO:1318
SEQ ID NO:566 and SEQ ID NO:1319
SEQ ID NO:567 and SEQ ID NO:1320
SEQ ID NO:569 and SEQ ID NO:1321
SEQ ID NO:570 and SEQ ID NO:1322
SEQ ID NO:571 and SEQ ID NO:1323
SEQ ID NO:572 and SEQ ID NO:1324
SEQ ID NO:573 and SEQ ID NO:1325
SEQ ID NO:574 and SEQ ID NO:1326
SEQ ID NO:575 and SEQ ID NO:1327
SEQ ID NO:576 and SEQ ID NO:1328
SEQ ID NO:577 and SEQ ID NO:1329
SEQ ID NO:579 and SEQ ID NO:1330
SEQ ID NO:580 and SEQ ID NO:1331
SEQ ID NO:581 and SEQ ID NO:1332
SEQ ID NO:582 and SEQ ID NO:1333
SEQ ID NO:583 and SEQ ID NO:1334
SEQ ID NO:584 and SEQ ID NO:1335
SEQ ID NO:585 and SEQ ID NO:1336

SEQ ID NO:586 and SEQ ID NO:1337
SEQ ID NO:587 and SEQ ID NO:1338
SEQ ID NO:588 and SEQ ID NO:1339
SEQ ID NO:589 and SEQ ID NO:1340
SEQ ID NO:590 and SEQ ID NO:1341
SEQ ID NO:591 and SEQ ID NO:1342
SEQ ID NO:592 and SEQ ID NO:1343
SEQ ID NO:593 and SEQ ID NO:1344
SEQ ID NO:594 and SEQ ID NO:1345
SEQ ID NO:595 and SEQ ID NO:1346
SEQ ID NO:596 and SEQ ID NO:1347
SEQ ID NO:597 and SEQ ID NO:1348
SEQ ID NO:598 and SEQ ID NO:1349
SEQ ID NO:599 and SEQ ID NO:1350
SEQ ID NO:600 and SEQ ID NO:1351
SEQ ID NO:601 and SEQ ID NO:1352
SEQ ID NO:602 and SEQ ID NO:1353
SEQ ID NO:603 and SEQ ID NO:1354
SEQ ID NO:604 and SEQ ID NO:1355
SEQ ID NO:605 and SEQ ID NO:1356
SEQ ID NO:606 and SEQ ID NO:1357
SEQ ID NO:607 and SEQ ID NO:1358
SEQ ID NO:608 and SEQ ID NO:1359
SEQ ID NO:609 and SEQ ID NO:1360
SEQ ID NO:610 and SEQ ID NO:1361
SEQ ID NO:611 and SEQ ID NO:1362
SEQ ID NO:612 and SEQ ID NO:1363
SEQ ID NO:613 and SEQ ID NO:1364
SEQ ID NO:614 and SEQ ID NO:1365
SEQ ID NO:615 and SEQ ID NO:1366
SEQ ID NO:616 and SEQ ID NO:1367
SEQ ID NO:617 and SEQ ID NO:1368
SEQ ID NO:618 and SEQ ID NO:1369
SEQ ID NO:619 and SEQ ID NO:1370
SEQ ID NO:620 and SEQ ID NO:1371
SEQ ID NO:621 and SEQ ID NO:1372
SEQ ID NO:622 and SEQ ID NO:1373
SEQ ID NO:623 and SEQ ID NO:1374
SEQ ID NO:624 and SEQ ID NO:1375
SEQ ID NO:625 and SEQ ID NO:1376
SEQ ID NO:626 and SEQ ID NO:1377
SEQ ID NO:627 and SEQ ID NO:1378
SEQ ID NO:628 and SEQ ID NO:1379
SEQ ID NO:629 and SEQ ID NO:1380
SEQ ID NO:630 and SEQ ID NO:1381
SEQ ID NO:631 and SEQ ID NO:1382
SEQ ID NO:632 and SEQ ID NO:1383
SEQ ID NO:633 and SEQ ID NO:1384
SEQ ID NO:634 and SEQ ID NO:1385
SEQ ID NO:635 and SEQ ID NO:1386
SEQ ID NO:636 and SEQ ID NO:1387
SEQ ID NO:637 and SEQ ID NO:1388

SEQ ID NO:638 and SEQ ID NO:1389
SEQ ID NO:639 and SEQ ID NO:1390
SEQ ID NO:640 and SEQ ID NO:1391
SEQ ID NO:641 and SEQ ID NO:1392
SEQ ID NO:642 and SEQ ID NO:1393
SEQ ID NO:643 and SEQ ID NO:1394
SEQ ID NO:644 and SEQ ID NO:1395
SEQ ID NO:645 and SEQ ID NO:1396
SEQ ID NO:646 and SEQ ID NO:1397
SEQ ID NO:647 and SEQ ID NO:1398
SEQ ID NO:648 and SEQ ID NO:1399
SEQ ID NO:649 and SEQ ID NO:1400
SEQ ID NO:650 and SEQ ID NO:1401
SEQ ID NO:651 and SEQ ID NO:1402
SEQ ID NO:652 and SEQ ID NO:1403
SEQ ID NO:653 and SEQ ID NO:1404
SEQ ID NO:654 and SEQ ID NO:1405
SEQ ID NO:655 and SEQ ID NO:1406
SEQ ID NO:656 and SEQ ID NO:1407
SEQ ID NO:657 and SEQ ID NO:1408
SEQ ID NO:658 and SEQ ID NO:1409
SEQ ID NO:659 and SEQ ID NO:1410
SEQ ID NO:660 and SEQ ID NO:1411
SEQ ID NO:661 and SEQ ID NO:1412
SEQ ID NO:662 and SEQ ID NO:1413
SEQ ID NO:663 and SEQ ID NO:1414
SEQ ID NO:664 and SEQ ID NO:1415
SEQ ID NO:665 and SEQ ID NO:1416
SEQ ID NO:666 and SEQ ID NO:1417
SEQ ID NO:667 and SEQ ID NO:1418
SEQ ID NO:668 and SEQ ID NO:1419
SEQ ID NO:669 and SEQ ID NO:1420
SEQ ID NO:670 and SEQ ID NO:1421
SEQ ID NO:671 and SEQ ID NO:1422
SEQ ID NO:672 and SEQ ID NO:1423
SEQ ID NO:673 and SEQ ID NO:1424
SEQ ID NO:674 and SEQ ID NO:1425
SEQ ID NO:675 and SEQ ID NO:1426
SEQ ID NO:676 and SEQ ID NO:1427
SEQ ID NO:677 and SEQ ID NO:1428
SEQ ID NO:678 and SEQ ID NO:1429
SEQ ID NO:679 and SEQ ID NO:1430
SEQ ID NO:680 and SEQ ID NO:1431
SEQ ID NO:681 and SEQ ID NO:1432
SEQ ID NO:682 and SEQ ID NO:1433
SEQ ID NO:683 and SEQ ID NO:1434
SEQ ID NO:684 and SEQ ID NO:1435
SEQ ID NO:685 and SEQ ID NO:1436
SEQ ID NO:686 and SEQ ID NO:1437
SEQ ID NO:687 and SEQ ID NO:1438
SEQ ID NO:688 and SEQ ID NO:1439
SEQ ID NO:689 and SEQ ID NO:1440

SEQ ID NO:690 and SEQ ID NO:1441
SEQ ID NO:691 and SEQ ID NO:1442
SEQ ID NO:692 and SEQ ID NO:1443
SEQ ID NO:693 and SEQ ID NO:1444
SEQ ID NO:694 and SEQ ID NO:1445
SEQ ID NO:695 and SEQ ID NO:1446
SEQ ID NO:696 and SEQ ID NO:1447
SEQ ID NO:697 and SEQ ID NO:1448
SEQ ID NO:698 and SEQ ID NO:1449
SEQ ID NO:699 and SEQ ID NO:1450
SEQ ID NO:700 and SEQ ID NO:1451
SEQ ID NO:701 and SEQ ID NO:1452
SEQ ID NO:702 and SEQ ID NO:1453
SEQ ID NO:703 and SEQ ID NO:1454
SEQ ID NO:704 and SEQ ID NO:1455
SEQ ID NO:705 and SEQ ID NO:1456
SEQ ID NO:706 and SEQ ID NO:1457
SEQ ID NO:707 and SEQ ID NO:1458
SEQ ID NO:708 and SEQ ID NO:1459
SEQ ID NO:709 and SEQ ID NO:1460
SEQ ID NO:710 and SEQ ID NO:1461
SEQ ID NO:711 and SEQ ID NO:1462
SEQ ID NO:712 and SEQ ID NO:1463
SEQ ID NO:713 and SEQ ID NO:1464
SEQ ID NO:714 and SEQ ID NO:1465
SEQ ID NO:715 and SEQ ID NO:1466
SEQ ID NO:716 and SEQ ID NO:1467
SEQ ID NO:717 and SEQ ID NO:1468
SEQ ID NO:718 and SEQ ID NO:1469
SEQ ID NO:719 and SEQ ID NO:1470
SEQ ID NO:720 and SEQ ID NO:1471
SEQ ID NO:721 and SEQ ID NO:1472
SEQ ID NO:722 and SEQ ID NO:1473
SEQ ID NO:723 and SEQ ID NO:1474
SEQ ID NO:724 and SEQ ID NO:1475
SEQ ID NO:725 and SEQ ID NO:1476
SEQ ID NO:726 and SEQ ID NO:1477
SEQ ID NO:727 and SEQ ID NO:1478
SEQ ID NO:729 and SEQ ID NO:1479
SEQ ID NO:730 and SEQ ID NO:1480
SEQ ID NO:731 and SEQ ID NO:1481
SEQ ID NO:732 and SEQ ID NO:1482
SEQ ID NO:733 and SEQ ID NO:1483
SEQ ID NO:734 and SEQ ID NO:1484
SEQ ID NO:735 and SEQ ID NO:1485
SEQ ID NO:736 and SEQ ID NO:1486
SEQ ID NO:737 and SEQ ID NO:1487
SEQ ID NO:738 and SEQ ID NO:1488
SEQ ID NO:739 and SEQ ID NO:1489
SEQ ID NO:740 and SEQ ID NO:1490
SEQ ID NO:741 and SEQ ID NO:1491
SEQ ID NO:745 and SEQ ID NO:1492

SEQ ID NO:746 and SEQ ID NO:1493
SEQ ID NO:747 and SEQ ID NO:1494
SEQ ID NO:748 and SEQ ID NO:1495
SEQ ID NO:749 and SEQ ID NO:1496
SEQ ID NO:750 and SEQ ID NO:1497
SEQ ID NO:751 and SEQ ID NO:1498
SEQ ID NO:752 and SEQ ID NO:1499
SEQ ID NO:753 and SEQ ID NO:1500
SEQ ID NO:754 and SEQ ID NO:1501
SEQ ID NO:755 and SEQ ID NO:1502
SEQ ID NO:756 and SEQ ID NO:1503
SEQ ID NO:757 and SEQ ID NO:1504
SEQ ID NO:758 and SEQ ID NO:1505
SEQ ID NO:759 and SEQ ID NO:1506
SEQ ID NO:760 and SEQ ID NO:1507
SEQ ID NO:761 and SEQ ID NO:1508
SEQ ID NO:762 and SEQ ID NO:1509
SEQ ID NO:763 and SEQ ID NO:1510
SEQ ID NO:764 and SEQ ID NO:1511
SEQ ID NO:765 and SEQ ID NO:1512
SEQ ID NO:766 and SEQ ID NO:1513
SEQ ID NO:767 and SEQ ID NO:1514
SEQ ID NO:768 and SEQ ID NO:1515
SEQ ID NO:769 and SEQ ID NO:1516
SEQ ID NO:770 and SEQ ID NO:1517
SEQ ID NO:771 and SEQ ID NO:1518
SEQ ID NO:772 and SEQ ID NO:1519
SEQ ID NO:773 and SEQ ID NO:1520
SEQ ID NO:774 and SEQ ID NO:1521
SEQ ID NO:775 and SEQ ID NO:1522
SEQ ID NO:776 and SEQ ID NO:1523
SEQ ID NO:777 and SEQ ID NO:1524
SEQ ID NO:778 and SEQ ID NO:1525
SEQ ID NO:779 and SEQ ID NO:1526
SEQ ID NO:780 and SEQ ID NO:1527
SEQ ID NO:781 and SEQ ID NO:1528
SEQ ID NO:782 and SEQ ID NO:1529
SEQ ID NO:783 and SEQ ID NO:1530
SEQ ID NO:784 and SEQ ID NO:1531
SEQ ID NO:785 and SEQ ID NO:1532
SEQ ID NO:786 and SEQ ID NO:1533
SEQ ID NO:787 and SEQ ID NO:1534
SEQ ID NO:788 and SEQ ID NO:1535
SEQ ID NO:789 and SEQ ID NO:1536
SEQ ID NO:790 and SEQ ID NO:1537
SEQ ID NO:791 and SEQ ID NO:1538
SEQ ID NO:792 and SEQ ID NO:1539
SEQ ID NO:793 and SEQ ID NO:1540
SEQ ID NO:794 and SEQ ID NO:1541
SEQ ID NO:795 and SEQ ID NO:1542
SEQ ID NO:797 and SEQ ID NO:1543
SEQ ID NO:798 and SEQ ID NO:1544

SEQ ID NO:799 and SEQ ID NO:1545
SEQ ID NO:800 and SEQ ID NO:1546
SEQ ID NO:801 and SEQ ID NO:1547
SEQ ID NO:802 and SEQ ID NO:1548
SEQ ID NO:803 and SEQ ID NO:1549
SEQ ID NO:804 and SEQ ID NO:1550
SEQ ID NO:805 and SEQ ID NO:1551
SEQ ID NO:806 and SEQ ID NO:1552
SEQ ID NO:807 and SEQ ID NO:1553
SEQ ID NO:809 and SEQ ID NO:1554
SEQ ID NO:810 and SEQ ID NO:1555
SEQ ID NO:811 and SEQ ID NO:1556
SEQ ID NO:812 and SEQ ID NO:1557
SEQ ID NO:813 and SEQ ID NO:1558
SEQ ID NO:814 and SEQ ID NO:1559
SEQ ID NO:816 and SEQ ID NO:1560
SEQ ID NO:817 and SEQ ID NO:1561
SEQ ID NO:818 and SEQ ID NO:1562
SEQ ID NO:819 and SEQ ID NO:1563
SEQ ID NO:820 and SEQ ID NO:1564
SEQ ID NO:822 and SEQ ID NO:1565
SEQ ID NO:823 and SEQ ID NO:1566
SEQ ID NO:824 and SEQ ID NO:1567
SEQ ID NO:825 and SEQ ID NO:1568
SEQ ID NO:826 and SEQ ID NO:1569
SEQ ID NO:827 and SEQ ID NO:1570
SEQ ID NO:828 and SEQ ID NO:1571
SEQ ID NO:829 and SEQ ID NO:1572, and
SEQ ID NO:2545 and SEQ ID NO:2546

4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.

5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.

6. A substantially pure protein encoded by polynucleotide of claim 4.

7. A partial peptide of the protein of claim 6.

8. An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following SEQ ID NOs:

SEQ ID NO:2547, SEQ ID NO:nnnn , SEQ ID NO:2551, SEQ ID NO:2553, SEQ ID NO:2555, SEQ ID NO:2557, SEQ ID NO:2558, SEQ ID NO:2560, SEQ ID NO:2562, SEQ ID NO:2564, SEQ ID NO:2566, SEQ ID NO:2568, SEQ ID NO:2570, SEQ ID NO:2572, SEQ ID NO:2574, SEQ ID NO:2576, SEQ ID NO:2578, SEQ ID NO:2580, SEQ ID NO:2581, SEQ ID NO:2583, SEQ ID NO:2584, SEQ ID NO:nnnn , SEQ ID NO:2588, SEQ ID NO:2590, SEQ ID NO:2592, SEQ ID NO:2594, SEQ ID NO:2596, SEQ ID NO:2598, SEQ ID NO:nnnn , SEQ ID NO:2602, SEQ ID NO:2604, SEQ ID NO:2606, SEQ ID NO:2607, SEQ ID NO:2609, SEQ ID NO:2611, SEQ ID NO:2613, SEQ ID NO:2615, SEQ ID NO:2617, SEQ ID NO:2619, SEQ ID NO:2621, SEQ ID NO:2623, SEQ ID NO:2625, SEQ ID NO:2627, SEQ ID NO:2629, SEQ ID NO:2630, SEQ ID NO:2632, SEQ ID NO:2634, SEQ ID NO:2636, SEQ ID NO:2638, SEQ ID NO:2640, SEQ ID NO:2642, SEQ ID NO:2644, SEQ ID NO:2646, SEQ ID NO:2648, SEQ ID NO:2650, SEQ ID NO:2652, SEQ ID NO:2654, SEQ ID NO:2656, SEQ ID NO:2658, SEQ ID NO:2660, SEQ ID NO:2662, SEQ ID NO:2664, SEQ ID NO:2666, SEQ ID NO:2668, SEQ ID NO:2670, SEQ ID NO:2672, SEQ ID NO:2674, SEQ ID NO:2676, SEQ ID NO:2678, SEQ ID NO:2680, SEQ ID NO:2681, SEQ ID NO:2683, SEQ ID NO:2685, SEQ ID NO:2686, SEQ ID NO:2688, SEQ ID NO:2690, SEQ ID NO:2692, SEQ ID NO:2694, SEQ ID NO:2696, SEQ ID NO:2698, SEQ ID NO:2700, SEQ ID NO:2702, SEQ ID NO:2704, SEQ ID NO:2706, SEQ ID NO:2708,

SEQ ID NO:2710, SEQ ID NO:2712, SEQ ID NO:2714, SEQ ID NO:2715, SEQ ID NO:2717, SEQ ID NO:2718, SEQ ID NO:2719, SEQ ID NO:2721, SEQ ID NO:2722, SEQ ID NO:2724, SEQ ID NO:2726, SEQ ID NO:2728, SEQ ID NO:2730, SEQ ID NO:2732, SEQ ID NO:2734 SEQ ID NO:2735, SEQ ID NO:2737, SEQ ID NO:2739, SEQ ID NO:nnnn , SEQ ID NO:2743, SEQ ID NO:2745, SEQ ID NO:2747, SEQ ID NO:2749, SEQ ID NO:2750, SEQ ID NO:2752, SEQ ID NO:2754, SEQ ID NO:2755, SEQ ID NO:2758, SEQ ID NO:2760, SEQ ID NO:2761, SEQ ID NO:nnnn , SEQ ID NO:2765, SEQ ID NO:2766, SEQ ID NO:2768, SEQ ID NO:2770, SEQ ID NO:2772, SEQ ID NO:2774, SEQ ID NO:2776, SEQ ID NO:2778, SEQ ID NO:2780, SEQ ID NO:2782, SEQ ID NO:2784, SEQ ID NO:2786, SEQ ID NO:2788, SEQ ID NO:2790, SEQ ID NO:2792, SEQ ID NO:2794, SEQ ID NO:2796, SEQ ID NO:2798, SEQ ID NO:2800, SEQ ID NO:2802, SEQ ID NO:2804, SEQ ID NO:2806, SEQ ID NO:2808, SEQ ID NO:2810, SEQ ID NO:2812, SEQ ID NO:2814, SEQ ID NO:2816, SEQ ID NO:2818, SEQ ID NO:2820, SEQ ID NO:2822, SEQ ID NO:2824, SEQ ID NO:2826, SEQ ID NO:2828, SEQ ID NO:2830, SEQ ID NO:2832, SEQ ID NO:2834, SEQ ID NO:2836, SEQ ID NO:2838, SEQ ID NO:2840, SEQ ID NO:2842, SEQ ID NO:2844, SEQ ID NO:2846, SEQ ID NO:2848, SEQ ID NO:2850, SEQ ID NO:2852, SEQ ID NO:2854, SEQ ID NO:2856, SEQ ID NO:2858, SEQ ID NO:2860, SEQ ID NO:2862, SEQ ID NO:2864, SEQ ID NO:2866, SEQ ID NO:2868, SEQ ID NO:2870, SEQ ID NO:2872, SEQ ID NO:2874, SEQ ID NO:2876, SEQ ID NO:2878, SEQ ID NO:2880, SEQ ID NO:2882, SEQ ID NO:2884, SEQ ID NO:2886, SEQ ID NO:2888, SEQ ID NO:2890, SEQ ID NO:2892, SEQ ID NO:2894, SEQ ID NO:2896, SEQ ID NO:2898, SEQ ID NO:2900, SEQ ID NO:2902, SEQ ID NO:2904, SEQ ID NO:2906, SEQ ID NO:2908, SEQ ID NO:2910, SEQ ID NO:2912, SEQ ID NO:2914, SEQ ID NO:2916, SEQ ID NO:2918, SEQ ID NO:2920, SEQ ID NO:2922, SEQ ID NO:2924, SEQ ID NO:2926, SEQ ID NO:2928, SEQ ID NO:2930 SEQ ID NO:2932, SEQ ID NO:2934, SEQ ID NO:2936, SEQ ID NO:2938, SEQ ID NO:2940, SEQ ID NO:2942, SEQ ID NO:2944, SEQ ID NO:2946, SEQ ID NO:2948, SEQ ID NO:2950, SEQ ID NO:2952, SEQ ID NO:2954, SEQ ID NO:2956, SEQ ID NO:2958, SEQ ID NO:2960, SEQ ID NO:2962, SEQ ID NO:nnnn , SEQ ID NO:2966, SEQ ID NO:2967, SEQ ID NO:2969, SEQ ID NO:2971, SEQ ID NO:2973, SEQ ID NO:2975, SEQ ID NO:2977, SEQ ID NO:2979, SEQ ID NO:2981, SEQ ID NO:2983, SEQ ID NO:2985, SEQ ID NO:2987, SEQ ID NO:2989, SEQ ID NO:2991, SEQ ID NO:2993, SEQ ID NO:2995, SEQ ID NO:2997, SEQ ID NO:2999, SEQ ID NO:3001, SEQ ID NO:3003, SEQ ID NO:3005, SEQ ID NO:3007, SEQ ID NO:3009, SEQ ID NO:3011, SEQ ID NO:3013, SEQ ID NO:3015, SEQ ID NO:3017, SEQ ID NO:3019, SEQ ID NO:3021, SEQ ID NO:3023, SEQ ID NO:3025, SEQ ID NO:3027, SEQ ID NO:3029, SEQ ID NO:3031, SEQ ID NO:3033, SEQ ID NO:3035, SEQ ID NO:3037, SEQ ID NO:3039, SEQ ID NO:nnnn , SEQ ID NO:nnnn , SEQ ID NO:3045, SEQ ID NO:3047, SEQ ID NO:3049, SEQ ID NO:3051, SEQ ID NO:3053, SEQ ID NO:3055, SEQ ID NO:3057, SEQ ID NO:3059, SEQ ID NO:3061, SEQ ID NO:3063, SEQ ID NO:3065, SEQ ID NO:3067, SEQ ID NO:3069, SEQ ID NO:3071, SEQ ID NO:3073, SEQ ID NO:3075, SEQ ID NO:3077, SEQ ID NO:3079, SEQ ID NO:3081, SEQ ID NO:3083, SEQ ID NO:3085, SEQ ID NO:3087, SEQ ID NO:3089, SEQ ID NO:3091, SEQ ID NO:3093, SEQ ID NO:3095, SEQ ID NO:3097, SEQ ID NO:3099, SEQ ID NO:3101, SEQ ID NO:3103, SEQ ID NO:3105, SEQ ID NO:3107, SEQ ID NO:3109, SEQ ID NO:3111, SEQ ID NO:3113, SEQ ID NO:3115, SEQ ID NO:3117, SEQ ID NO:3119, SEQ ID NO:3121, SEQ ID NO:3123, SEQ ID NO:3125, SEQ ID NO:3127, SEQ ID NO:3129 SEQ ID NO:3131, SEQ ID NO:3133, SEQ ID NO:3135, SEQ ID NO:3137, SEQ ID NO:3139, SEQ ID NO:3140, SEQ ID NO:3142, SEQ ID NO:3143, SEQ ID NO:3144, SEQ ID NO:3146, SEQ ID NO:3148, SEQ ID NO:3150, SEQ ID NO:3152, SEQ ID NO:3154, SEQ ID NO:3156, SEQ ID NO:3158, SEQ ID NO:nnnn , SEQ ID NO:3162, SEQ ID NO:3164, SEQ ID NO:3166, SEQ ID NO:3168, SEQ ID NO:3170, SEQ ID NO:3172, SEQ ID NO:3174, SEQ ID NO:3176, SEQ ID NO:3178, SEQ ID NO:3180, SEQ ID NO:3181, SEQ ID NO:3183, SEQ ID NO:3185, SEQ ID NO:3187, SEQ ID NO:3188, SEQ ID NO:3189, SEQ ID NO:3191, SEQ ID NO:3193, SEQ ID NO:3195, SEQ ID NO:3196, SEQ ID NO:3198, SEQ ID NO:3200, SEQ ID NO:3202, SEQ ID NO:3204, SEQ ID NO:3206, SEQ ID NO:3208, SEQ ID NO:3210, SEQ ID NO:3212,

SEQ ID NO:3214, SEQ ID NO:nnnn , SEQ ID NO:3218, SEQ ID NO:3219, SEQ ID NO:3221, SEQ ID NO:3222, SEQ ID NO:3224, SEQ ID NO:3226, SEQ ID NO:nnnn , SEQ ID NO:3230, SEQ ID NO:3232, SEQ ID NO:3234, SEQ ID NO:3236, SEQ ID NO:3238, SEQ ID NO:3240, SEQ ID NO:3242, SEQ ID NO:3244, SEQ ID NO:3246, SEQ ID NO:nnnn , SEQ ID NO:3250, SEQ ID NO:3252, SEQ ID NO:3254, SEQ ID NO:3256, SEQ ID NO:3258, SEQ ID NO:3260, SEQ ID NO:3262, SEQ ID NO:3264, SEQ ID NO:3266, SEQ ID NO:3268, SEQ ID NO:3270, SEQ ID NO:3272, SEQ ID NO:3274, SEQ ID NO:3276, SEQ ID NO:3278, SEQ ID NO:3280, SEQ ID NO:3282, SEQ ID NO:3284, SEQ ID NO:3286, SEQ ID NO:3288, SEQ ID NO:3290, SEQ ID NO:3292, SEQ ID NO:3294, SEQ ID NO:3296, SEQ ID NO:3298, SEQ ID NO:3300, SEQ ID NO:3301, SEQ ID NO:3303, SEQ ID NO:3305, SEQ ID NO:3307, SEQ ID NO:3309, SEQ ID NO:3311, SEQ ID NO:3312, SEQ ID NO:3314, SEQ ID NO:3316, SEQ ID NO:3318 SEQ ID NO:3320, SEQ ID NO:3322, SEQ ID NO:3324, SEQ ID NO:3326, SEQ ID NO:3328, SEQ ID NO:3330, SEQ ID NO:3332, SEQ ID NO:3334, SEQ ID NO:3336, SEQ ID NO:3338, SEQ ID NO:nnnn , SEQ ID NO:3342, SEQ ID NO:3344, SEQ ID NO:3346, SEQ ID NO:3348, SEQ ID NO:3350, SEQ ID NO:3352, SEQ ID NO:3354, SEQ ID NO:3356, SEQ ID NO:3358, SEQ ID NO:3360, SEQ ID NO:3362, SEQ ID NO:3364, SEQ ID NO:3366, SEQ ID NO:3368, SEQ ID NO:3370, SEQ ID NO:3372, SEQ ID NO:3374, SEQ ID NO:3376, SEQ ID NO:3378, SEQ ID NO:3380, SEQ ID NO:3382, SEQ ID NO:3384, SEQ ID NO:3386, SEQ ID NO:3388, SEQ ID NO:3390, SEQ ID NO:3392, SEQ ID NO:3394, SEQ ID NO:3396, SEQ ID NO:3398, SEQ ID NO:3400, SEQ ID NO:3402, SEQ ID NO:3404, SEQ ID NO:nnnn , SEQ ID NO:3408, SEQ ID NO:3410, SEQ ID NO:3411, SEQ ID NO:3413, SEQ ID NO:3415, SEQ ID NO:3417, SEQ ID NO:3419, SEQ ID NO:nnnn , SEQ ID NO:3423, SEQ ID NO:3425, SEQ ID NO:3427, SEQ ID NO:3429, SEQ ID NO:3431, SEQ ID NO:3433, SEQ ID NO:3435, SEQ ID NO:3437, SEQ ID NO:3439, SEQ ID NO:3441, SEQ ID NO:3443, SEQ ID NO:3445, SEQ ID NO:3447, SEQ ID NO:3449, SEQ ID NO:3451, SEQ ID NO:3453, SEQ ID NO:3455, SEQ ID NO:3457, SEQ ID NO:3459, SEQ ID NO:3461, SEQ ID NO:3463, SEQ ID NO:3465, SEQ ID NO:3467, SEQ ID NO:3469, SEQ ID NO:3471, SEQ ID NO:3473, SEQ ID NO:3475, SEQ ID NO:3477, SEQ ID NO:3479, SEQ ID NO:3481, SEQ ID NO:3482, SEQ ID NO:3484, SEQ ID NO:3486, SEQ ID NO:3488, SEQ ID NO:3490, SEQ ID NO:3492, SEQ ID NO:3494, SEQ ID NO:3496, SEQ ID NO:3498, SEQ ID NO:3500, SEQ ID NO:3502, SEQ ID NO:3504, SEQ ID NO:3506, SEQ ID NO:3508, SEQ ID NO:3509, SEQ ID NO:3511, SEQ ID NO:3513, SEQ ID NO:3515 SEQ ID NO:3517, SEQ ID NO:3519, SEQ ID NO:3521, SEQ ID NO:3523, SEQ ID NO:3525, SEQ ID NO:3527, SEQ ID NO:3529, SEQ ID NO:3531, SEQ ID NO:3533, SEQ ID NO:3535, SEQ ID NO:3537, SEQ ID NO:3539, SEQ ID NO:3541, SEQ ID NO:3543, SEQ ID NO:3545, SEQ ID NO:3547, SEQ ID NO:3549, SEQ ID NO:3551, SEQ ID NO:3553, SEQ ID NO:3555, SEQ ID NO:3557, SEQ ID NO:3559, SEQ ID NO:3561, SEQ ID NO:3563, SEQ ID NO:nnnn , SEQ ID NO:3567, SEQ ID NO:3569, SEQ ID NO:3571, SEQ ID NO:3573, SEQ ID NO:3575, SEQ ID NO:3577, SEQ ID NO:3579, SEQ ID NO:3581, SEQ ID NO:3583, SEQ ID NO:3585, SEQ ID NO:3587, SEQ ID NO:3589 , SEQ ID NO:3595, SEQ ID NO:3597, SEQ ID NO:3599, SEQ ID NO:3601, SEQ ID NO:3603, SEQ ID NO:3605, SEQ ID NO:3607, SEQ ID NO:3609, SEQ ID NO:3610, SEQ ID NO:3611, SEQ ID NO:3612, SEQ ID NO:3613, SEQ ID NO:3615, SEQ ID NO:3617, SEQ ID NO:3619, SEQ ID NO:3621, SEQ ID NO:3622, SEQ ID NO:3624, SEQ ID NO:3626, SEQ ID NO:3627, SEQ ID NO:3628, SEQ ID NO:3629, SEQ ID NO:3631, SEQ ID NO:3633, SEQ ID NO:3634, SEQ ID NO:3636, SEQ ID NO:3638, SEQ ID NO:3640, SEQ ID NO:3642, SEQ ID NO:3644, SEQ ID NO:3645, SEQ ID NO:3647, SEQ ID NO:3649, SEQ ID NO:3651, SEQ ID NO:3653, SEQ ID NO:3655, SEQ ID NO:3657, SEQ ID NO:3658, SEQ ID NO:3660, SEQ ID NO:3662, SEQ ID NO:3664, SEQ ID NO:3666, SEQ ID NO:3668, SEQ ID NO:3670, SEQ ID NO:3672, SEQ ID NO:3674, SEQ ID NO:3676, SEQ ID NO:3678, SEQ ID NO:3680, SEQ ID NO:3682, SEQ ID NO:3683, SEQ ID NO:3685, SEQ ID NO:3686, SEQ ID NO:3688, SEQ ID NO:3690, SEQ ID NO:3692, SEQ ID NO:3694, SEQ ID NO:3696, SEQ ID NO:3698, SEQ ID NO:3700, SEQ ID NO:3702, SEQ ID NO:3704, SEQ ID NO:3706, SEQ ID NO:3708, SEQ ID NO:3710, SEQ ID NO:3712, SEQ ID NO:3714, SEQ ID NO:3716,

SEQ ID NO:3718, SEQ ID NO:3720, SEQ ID NO:3722, SEQ ID NO:3724, SEQ ID NO:3726, SEQ ID NO:3728, SEQ ID NO:3730, SEQ ID NO:3732, SEQ ID NO:3734, SEQ ID NO:3736, SEQ ID NO:3738, SEQ ID NO:3740, SEQ ID NO:3741, SEQ ID NO:3743, SEQ ID NO:3745, SEQ ID NO:3747, SEQ ID NO:3749, SEQ ID NO:3751, SEQ ID NO:3753, SEQ ID NO:3755, SEQ ID NO:3756, SEQ ID NO:3758, SEQ ID NO:3760, SEQ ID NO:3761, SEQ ID NO:3763, SEQ ID NO:3765, SEQ ID NO:3767, SEQ ID NO:3769, SEQ ID NO:3771, SEQ ID NO:3773, SEQ ID NO:3775, SEQ ID NO:3777

SEQ ID NO:3779, SEQ ID NO:3781, SEQ ID NO:3783, SEQ ID NO:3785, SEQ ID NO:3787, SEQ ID NO:3789, SEQ ID NO:3791, SEQ ID NO:3793, SEQ ID NO:3795, SEQ ID NO:3797, SEQ ID NO:3799, SEQ ID NO:3801, SEQ ID NO:3803, SEQ ID NO:3805, SEQ ID NO:3806, SEQ ID NO:3808, SEQ ID NO:3810, SEQ ID NO:3812, SEQ ID NO:3814, SEQ ID NO:3816, SEQ ID NO:3818, SEQ ID NO:3820, SEQ ID NO:3822, SEQ ID NO:3824, SEQ ID NO:3826, SEQ ID NO:3828, SEQ ID NO:3830, SEQ ID NO:3832, SEQ ID NO:3834, SEQ ID NO:3836, SEQ ID NO:3838, SEQ ID NO:3840, SEQ ID NO:3842, SEQ ID NO:3844, SEQ ID NO:3846, SEQ ID NO:3848, SEQ ID NO:3852, SEQ ID NO:3854, SEQ ID NO:3856, SEQ ID NO:3858, SEQ ID NO:3860, SEQ ID NO:3862, SEQ ID NO:3864, SEQ ID NO:3866, SEQ ID NO:3868, SEQ ID NO:3870, SEQ ID NO:3872, SEQ ID NO:3874, SEQ ID NO:3876, SEQ ID NO:3878, SEQ ID NO:3880, SEQ ID NO:3882, SEQ ID NO:3884, SEQ ID NO:3886, SEQ ID NO:3888, SEQ ID NO:3890, SEQ ID NO:3892, SEQ ID NO:3894, SEQ ID NO:3896, SEQ ID NO:3898, SEQ ID NO:3900, SEQ ID NO:3902, SEQ ID NO:3904, SEQ ID NO:3906, SEQ ID NO:3908, SEQ ID NO:3910, SEQ ID NO:3912, SEQ ID NO:3914, SEQ ID NO:3916, SEQ ID NO:3918, SEQ ID NO:3920, SEQ ID NO:3922, SEQ ID NO:3924, SEQ ID NO:3926, SEQ ID NO:3928, SEQ ID NO:3930, SEQ ID NO:3932, SEQ ID NO:3934, SEQ ID NO:3936, SEQ ID NO:3938, SEQ ID NO:3940, SEQ ID NO:3942, SEQ ID NO:3944, SEQ ID NO:3946, SEQ ID NO:3948, SEQ ID NO:3950, SEQ ID NO:3952, SEQ ID NO:3954, SEQ ID NO:3956, SEQ ID NO:3958, SEQ ID NO:3960, SEQ ID NO:3962, SEQ ID NO:3964, SEQ ID NO:3965, SEQ ID NO:3966, SEQ ID NO:3968, SEQ ID NO:3970, SEQ ID NO:3972, SEQ ID NO:3974, SEQ ID NO:3976 SEQ ID NO:3977, SEQ ID NO:3979, SEQ ID NO:3981, SEQ ID NO:3983, SEQ ID NO:3985, SEQ ID NO:3987, SEQ ID NO:3988, SEQ ID NO:3990, SEQ ID NO:3992, SEQ ID NO:3994, SEQ ID NO:3996, SEQ ID NO:3998, SEQ ID NO:4000, SEQ ID NO:4001, SEQ ID NO:4003, SEQ ID NO:4004, SEQ ID NO:4006, SEQ ID NO:4008, SEQ ID NO:4010, SEQ ID NO:4012, SEQ ID NO:4016, SEQ ID NO:4018, SEQ ID NO:4020, SEQ ID NO:4022, SEQ ID NO:4024, SEQ ID NO:4026, SEQ ID NO:4028, SEQ ID NO:4030, SEQ ID NO:4032, SEQ ID NO:4034, SEQ ID NO:4036, SEQ ID NO:4038, SEQ ID NO:4040, SEQ ID NO:4042, SEQ ID NO:4044, SEQ ID NO:4046, SEQ ID NO:4048, SEQ ID NO:4050, SEQ ID NO:4052, SEQ ID NO:4054, SEQ ID NO:4056, SEQ ID NO:4058, SEQ ID NO:4060, SEQ ID NO:4062, SEQ ID NO:4064, SEQ ID NO:4066, SEQ ID NO:4068, SEQ ID NO:4070, SEQ ID NO:4072, SEQ ID NO:4074, SEQ ID NO:4076

SEQ ID NO:4078, SEQ ID NO:4080, SEQ ID NO:4082, SEQ ID NO:4084, SEQ ID NO:4086, SEQ ID NO:4088, SEQ ID NO:4090, SEQ ID NO:4092, SEQ ID NO:4094, SEQ ID NO:4096, SEQ ID NO:4098, SEQ ID NO:4099, SEQ ID NO:4101, SEQ ID NO:4103, SEQ ID NO:4105, SEQ ID NO:4107, SEQ ID NO:4109, SEQ ID NO:4111, SEQ ID NO:4113, SEQ ID NO:4115, SEQ ID NO:4117, SEQ ID NO:4119, SEQ ID NO:4121, SEQ ID NO:4123, SEQ ID NO:4125, SEQ ID NO:4127, SEQ ID NO:4129, SEQ ID NO:4131, SEQ ID NO:4132, SEQ ID NO:4134, SEQ ID NO:4136, SEQ ID NO:4137, SEQ ID NO:4139, SEQ ID NO:4140, SEQ ID NO:4142, SEQ ID NO:4144, SEQ ID NO:4146, SEQ ID NO:4148, SEQ ID NO:4150, SEQ ID NO:4152, SEQ ID NO:4154, SEQ ID NO:4155, SEQ ID NO:4157, SEQ ID NO:4159, SEQ ID NO:4161, SEQ ID NO:4163, SEQ ID NO:4165

SEQ ID NO:4167, SEQ ID NO:4168, SEQ ID NO:4170, SEQ ID NO:4172, SEQ ID NO:4174, SEQ ID NO:4176, and SEQ ID NO:4178

(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence

set forth in any one of the following SEQ ID NOs:

SEQ ID NO:2548, SEQ ID NO:nnnn , SEQ ID NO:2552, SEQ ID NO:2554, SEQ ID NO:2556, SEQ ID NO:2559, SEQ ID NO:2561, SEQ ID NO:2563, SEQ ID NO:2565, SEQ ID NO:2567, SEQ ID NO:2569, SEQ ID NO:2571, SEQ ID NO:2573, SEQ ID NO:2575, SEQ ID NO:2577, SEQ ID NO:2579, SEQ ID NO:2582, SEQ ID NO:2585, SEQ ID NO:nnnn , SEQ ID NO:2589, SEQ ID NO:2591, SEQ ID NO:2593, SEQ ID NO:2595, SEQ ID NO:2597, SEQ ID NO:2599, SEQ ID NO:nnnn , SEQ ID NO:2603, SEQ ID NO:2605, SEQ ID NO:2608, SEQ ID NO:2610, SEQ ID NO:2612, SEQ ID NO:2614, SEQ ID NO:2616, SEQ ID NO:2618, SEQ ID NO:2620, SEQ ID NO:2622, SEQ ID NO:2624, SEQ ID NO:2626, SEQ ID NO:2628, SEQ ID NO:2631, SEQ ID NO:2633, SEQ ID NO:2635, SEQ ID NO:2637, SEQ ID NO:2639, SEQ ID NO:2641, SEQ ID NO:2643, SEQ ID NO:2645, SEQ ID NO:2647, SEQ ID NO:2649, SEQ ID NO:2651, SEQ ID NO:2653, SEQ ID NO:2655, SEQ ID NO:2657, SEQ ID NO:2659, SEQ ID NO:2661, SEQ ID NO:2663, SEQ ID NO:2665, SEQ ID NO:2667, SEQ ID NO:2669, SEQ ID NO:2671, SEQ ID NO:2673, SEQ ID NO:2675, SEQ ID NO:2677, SEQ ID NO:2679, SEQ ID NO:2682, SEQ ID NO:2684, SEQ ID NO:2687, SEQ ID NO:2689, SEQ ID NO:2691, SEQ ID NO:2693, SEQ ID NO:2695, SEQ ID NO:2697, SEQ ID NO:2699, SEQ ID NO:2701, SEQ ID NO:2703, SEQ ID NO:2705, SEQ ID NO:2707, SEQ ID NO:2709, SEQ ID NO:2711, SEQ ID NO:2713, SEQ ID NO:2716, SEQ ID NO:2720, SEQ ID NO:2723, SEQ ID NO:2725, SEQ ID NO:2727, SEQ ID NO:2729, SEQ ID NO:2731, SEQ ID NO:2733, SEQ ID NO:2736, SEQ ID NO:2738, SEQ ID NO:2740, SEQ ID NO:nnnn , SEQ ID NO:2744, SEQ ID NO:2746, SEQ ID NO:2748, SEQ ID NO:2751, SEQ ID NO:2753, SEQ ID NO:2755, SEQ ID NO:2757, SEQ ID NO:2759 SEQ ID NO:2762, SEQ ID NO:nnnn , SEQ ID NO:2767, SEQ ID NO:2769, SEQ ID NO:2771, SEQ ID NO:2773, SEQ ID NO:2775, SEQ ID NO:2777, SEQ ID NO:2779, SEQ ID NO:2781, SEQ ID NO:2783, SEQ ID NO:2785, SEQ ID NO:2787, SEQ ID NO:2789, SEQ ID NO:2791, SEQ ID NO:2793, SEQ ID NO:2795, SEQ ID NO:2797, SEQ ID NO:2799, SEQ ID NO:2801, SEQ ID NO:2803, SEQ ID NO:2805, SEQ ID NO:2807, SEQ ID NO:2809, SEQ ID NO:2811, SEQ ID NO:2813, SEQ ID NO:2815, SEQ ID NO:2817, SEQ ID NO:2819, SEQ ID NO:2821, SEQ ID NO:2823, SEQ ID NO:2825, SEQ ID NO:2827, SEQ ID NO:2829, SEQ ID NO:2831, SEQ ID NO:2833, SEQ ID NO:2835, SEQ ID NO:2837, SEQ ID NO:2839, SEQ ID NO:2841, SEQ ID NO:2843, SEQ ID NO:2845, SEQ ID NO:2847, SEQ ID NO:2849, SEQ ID NO:2851, SEQ ID NO:2853, SEQ ID NO:2855, SEQ ID NO:2857, SEQ ID NO:2859, SEQ ID NO:2861, SEQ ID NO:2863, SEQ ID NO:2865, SEQ ID NO:2867, SEQ ID NO:2869, SEQ ID NO:2871, SEQ ID NO:2873, SEQ ID NO:2875, SEQ ID NO:2877, SEQ ID NO:2879, SEQ ID NO:2881, SEQ ID NO:2883, SEQ ID NO:2885, SEQ ID NO:2887, SEQ ID NO:2889, SEQ ID NO:2891, SEQ ID NO:2893, SEQ ID NO:2895, SEQ ID NO:2897, SEQ ID NO:2899, SEQ ID NO:2901, SEQ ID NO:2903, SEQ ID NO:2905, SEQ ID NO:2907, SEQ ID NO:2909, SEQ ID NO:2911, SEQ ID NO:2913, SEQ ID NO:2915, SEQ ID NO:2917, SEQ ID NO:2919, SEQ ID NO:2921, SEQ ID NO:2923, SEQ ID NO:2925, SEQ ID NO:2927, SEQ ID NO:2929, SEQ ID NO:2931, SEQ ID NO:2933, SEQ ID NO:2935, SEQ ID NO:2937, SEQ ID NO:2939, SEQ ID NO:2941, SEQ ID NO:2943, SEQ ID NO:2945, SEQ ID NO:2947, SEQ ID NO:2949, SEQ ID NO:2951, SEQ ID NO:2953, SEQ ID NO:2955, SEQ ID NO:2957, SEQ ID NO:2959, SEQ ID NO:2961 SEQ ID NO:2963, SEQ ID NO:nnnn , SEQ ID NO:2968, SEQ ID NO:2970, SEQ ID NO:2972, SEQ ID NO:2974, SEQ ID NO:2976, SEQ ID NO:2978, SEQ ID NO:2980, SEQ ID NO:2982, SEQ ID NO:2984, SEQ ID NO:2986, SEQ ID NO:2988, SEQ ID NO:2990, SEQ ID NO:2992, SEQ ID NO:2994, SEQ ID NO:2996, SEQ ID NO:2998, SEQ ID NO:3000, SEQ ID NO:3002, SEQ ID NO:3004, SEQ ID NO:3006, SEQ ID NO:3008, SEQ ID NO:3010, SEQ ID NO:3012, SEQ ID NO:3014, SEQ ID NO:3016, SEQ ID NO:3018, SEQ ID NO:3020, SEQ ID NO:3022, SEQ ID NO:3024, SEQ ID NO:3026, SEQ ID NO:3028, SEQ ID NO:3030, SEQ ID NO:3032, SEQ ID NO:3034, SEQ ID NO:3036, SEQ ID NO:3038, SEQ ID NO:3040, SEQ ID NO:nnnn , SEQ ID NO:nnnn , SEQ ID NO:3046, SEQ ID NO:3048, SEQ ID NO:3050, SEQ ID NO:3052, SEQ ID NO:3054, SEQ ID NO:3056, SEQ ID NO:3058, SEQ ID NO:3060, SEQ ID NO:3062, SEQ ID NO:3064, SEQ ID NO:3066, SEQ ID NO:3068, SEQ ID NO:3070, SEQ ID NO:3072, SEQ ID NO:3074, SEQ ID NO:3076, SEQ ID NO:3078, SEQ ID NO:3080, SEQ ID NO:3082,

SEQ ID NO:3084, SEQ ID NO:3086, SEQ ID NO:3088, SEQ ID NO:3090, SEQ ID NO:3092, SEQ ID NO:3094, SEQ ID NO:3096, SEQ ID NO:3098, SEQ ID NO:3100, SEQ ID NO:3102, SEQ ID NO:3104, SEQ ID NO:3106, SEQ ID NO:3108, SEQ ID NO:3110, SEQ ID NO:3112, SEQ ID NO:3114, SEQ ID NO:3116, SEQ ID NO:3118, SEQ ID NO:3120, SEQ ID NO:3122, SEQ ID NO:3124, SEQ ID NO:3126, SEQ ID NO:3128, SEQ ID NO:3130, SEQ ID NO:3132, SEQ ID NO:3134, SEQ ID NO:3136, SEQ ID NO:3138, SEQ ID NO:3141, SEQ ID NO:3145, SEQ ID NO:3147, SEQ ID NO:3149, SEQ ID NO:3151, SEQ ID NO:3153, SEQ ID NO:3155, SEQ ID NO:3157, SEQ ID NO:3159, SEQ ID NO:nnnn , SEQ ID NO:3163, SEQ ID NO:3165 SEQ ID NO:3167, SEQ ID NO:3169, SEQ ID NO:3171, SEQ ID NO:3173, SEQ ID NO:3175, SEQ ID NO:3177, SEQ ID NO:3179, SEQ ID NO:3182, SEQ ID NO:3184, SEQ ID NO:3186, SEQ ID NO:3190, SEQ ID NO:3192, SEQ ID NO:3194, SEQ ID NO:3197, SEQ ID NO:3199, SEQ ID NO:3201, SEQ ID NO:3203, SEQ ID NO:3205, SEQ ID NO:3207, SEQ ID NO:3209, SEQ ID NO:3211, SEQ ID NO:3213, SEQ ID NO:3215, SEQ ID NO:nnnn , SEQ ID NO:3220, SEQ ID NO:3223, SEQ ID NO:3225, SEQ ID NO:3227, SEQ ID NO:nnnn , SEQ ID NO:3231, SEQ ID NO:3233, SEQ ID NO:3235, SEQ ID NO:3237, SEQ ID NO:3239, SEQ ID NO:3241, SEQ ID NO:3243, SEQ ID NO:3245, SEQ ID NO:3247, SEQ ID NO:nnnn , SEQ ID NO:3251, SEQ ID NO:3253, SEQ ID NO:3255, SEQ ID NO:3257, SEQ ID NO:3259, SEQ ID NO:3261, SEQ ID NO:3263, SEQ ID NO:3265, SEQ ID NO:3267, SEQ ID NO:3269, SEQ ID NO:3271, SEQ ID NO:3273, SEQ ID NO:3275, SEQ ID NO:3277, SEQ ID NO:3279, SEQ ID NO:3281, SEQ ID NO:3283, SEQ ID NO:3285, SEQ ID NO:3287, SEQ ID NO:3289, SEQ ID NO:3291, SEQ ID NO:3293, SEQ ID NO:3295, SEQ ID NO:3297, SEQ ID NO:3299, SEQ ID NO:3302, SEQ ID NO:3304, SEQ ID NO:3306, SEQ ID NO:3308, SEQ ID NO:3310, SEQ ID NO:3313, SEQ ID NO:3315, SEQ ID NO:3317, SEQ ID NO:3319, SEQ ID NO:3321, SEQ ID NO:3323, SEQ ID NO:3325, SEQ ID NO:3327, SEQ ID NO:3329, SEQ ID NO:3331, SEQ ID NO:3333, SEQ ID NO:3335, SEQ ID NO:3337, SEQ ID NO:3339, SEQ ID NO:nnnn , SEQ ID NO:3343, SEQ ID NO:3345, SEQ ID NO:3347, SEQ ID NO:3349, SEQ ID NO:3351, SEQ ID NO:3353, SEQ ID NO:3355, SEQ ID NO:3357, SEQ ID NO:3359, SEQ ID NO:3361, SEQ ID NO:3363, SEQ ID NO:3365, SEQ ID NO:3367, SEQ ID NO:3369, SEQ ID NO:3371, SEQ ID NO:3373 SEQ ID NO:3375, SEQ ID NO:3377, SEQ ID NO:3379, SEQ ID NO:3381, SEQ ID NO:3383, SEQ ID NO:3385, SEQ ID NO:3387, SEQ ID NO:3389, SEQ ID NO:3391, SEQ ID NO:3393, SEQ ID NO:3395, SEQ ID NO:3397, SEQ ID NO:3399, SEQ ID NO:3401, SEQ ID NO:3403, SEQ ID NO:3405, SEQ ID NO:nnnn , SEQ ID NO:3409, SEQ ID NO:3412, SEQ ID NO:3414, SEQ ID NO:3416, SEQ ID NO:3418, SEQ ID NO:3420, SEQ ID NO:nnnn , SEQ ID NO:3424, SEQ ID NO:3426, SEQ ID NO:3428, SEQ ID NO:3430, SEQ ID NO:3432, SEQ ID NO:3434, SEQ ID NO:3436, SEQ ID NO:3438, SEQ ID NO:3440, SEQ ID NO:3442, SEQ ID NO:3444, SEQ ID NO:3446, SEQ ID NO:3448, SEQ ID NO:3450, SEQ ID NO:3452, SEQ ID NO:3454, SEQ ID NO:3456, SEQ ID NO:3458, SEQ ID NO:3460, SEQ ID NO:3462, SEQ ID NO:3464, SEQ ID NO:3466, SEQ ID NO:3468, SEQ ID NO:3470, SEQ ID NO:3472, SEQ ID NO:3474, SEQ ID NO:3476, SEQ ID NO:3478, SEQ ID NO:3480, SEQ ID NO:3483, SEQ ID NO:3485, SEQ ID NO:3487, SEQ ID NO:3489, SEQ ID NO:3491, SEQ ID NO:3493, SEQ ID NO:3495, SEQ ID NO:3497, SEQ ID NO:3499, SEQ ID NO:3501, SEQ ID NO:3503, SEQ ID NO:3505, SEQ ID NO:3507, SEQ ID NO:3510, SEQ ID NO:3512, SEQ ID NO:3514, SEQ ID NO:3516, SEQ ID NO:3518, SEQ ID NO:3520, SEQ ID NO:3522, SEQ ID NO:3524, SEQ ID NO:3526, SEQ ID NO:3528, SEQ ID NO:3530, SEQ ID NO:3532, SEQ ID NO:3534, SEQ ID NO:3536, SEQ ID NO:3538, SEQ ID NO:3540, SEQ ID NO:3542, SEQ ID NO:3544, SEQ ID NO:3546, SEQ ID NO:3548, SEQ ID NO:3550, SEQ ID NO:3552, SEQ ID NO:3554, SEQ ID NO:3556, SEQ ID NO:3558, SEQ ID NO:3560, SEQ ID NO:3562, SEQ ID NO:3564, SEQ ID NO:nnnn , SEQ ID NO:3568, SEQ ID NO:3570, SEQ ID NO:3572, SEQ ID NO:3574, SEQ ID NO:3576 SEQ ID NO:3578, SEQ ID NO:3580, SEQ ID NO:3582, SEQ ID NO:3584, SEQ ID NO:3586, SEQ ID NO:3588, SEQ ID NO:3590
SEQ ID NO:3596, SEQ ID NO:3598, SEQ ID NO:3600, SEQ ID NO:3602, SEQ ID NO:3604, SEQ ID NO:3606, SEQ ID NO:3608, SEQ ID NO:3614, SEQ ID NO:3616, SEQ ID NO:3618,

SEQ ID NO:3620, SEQ ID NO:3623, SEQ ID NO:3625, SEQ ID NO:3630, SEQ ID NO:3632, SEQ ID NO:3635, SEQ ID NO:3637, SEQ ID NO:3639, SEQ ID NO:3641, SEQ ID NO:3643, SEQ ID NO:3646, SEQ ID NO:3648, SEQ ID NO:3650, SEQ ID NO:3652, SEQ ID NO:3654, SEQ ID NO:3656, SEQ ID NO:3659, SEQ ID NO:3661, SEQ ID NO:3663, SEQ ID NO:3665, SEQ ID NO:3667, SEQ ID NO:3669, SEQ ID NO:3671, SEQ ID NO:3673, SEQ ID NO:3675, SEQ ID NO:3677, SEQ ID NO:3679, SEQ ID NO:3681, SEQ ID NO:3684, SEQ ID NO:3687, SEQ ID NO:3689, SEQ ID NO:3691, SEQ ID NO:3693, SEQ ID NO:3695, SEQ ID NO:3697, SEQ ID NO:3699, SEQ ID NO:3701, SEQ ID NO:3703, SEQ ID NO:3705, SEQ ID NO:3707, SEQ ID NO:3709, SEQ ID NO:3711, SEQ ID NO:3713, SEQ ID NO:3715, SEQ ID NO:3717, SEQ ID NO:3719, SEQ ID NO:3721, SEQ ID NO:3723, SEQ ID NO:3725, SEQ ID NO:3727, SEQ ID NO:3729, SEQ ID NO:3731, SEQ ID NO:3733, SEQ ID NO:3735, SEQ ID NO:3737, SEQ ID NO:3739, SEQ ID NO:3742, SEQ ID NO:3744, SEQ ID NO:3746, SEQ ID NO:3748, SEQ ID NO:3750, SEQ ID NO:3752, SEQ ID NO:3754, SEQ ID NO:3757, SEQ ID NO:3759, SEQ ID NO:3762, SEQ ID NO:3764, SEQ ID NO:3766, SEQ ID NO:3768, SEQ ID NO:3770, SEQ ID NO:3772, SEQ ID NO:3774, SEQ ID NO:3776, SEQ ID NO:3778, SEQ ID NO:3780, SEQ ID NO:3782, SEQ ID NO:3784, SEQ ID NO:3786, SEQ ID NO:3788, SEQ ID NO:3790, SEQ ID NO:3792, SEQ ID NO:3794, SEQ ID NO:3796, SEQ ID NO:3798, SEQ ID NO:3800, SEQ ID NO:3802, SEQ ID NO:3804, SEQ ID NO:3807, SEQ ID NO:3809, SEQ ID NO:3811 SEQ ID NO:3813, SEQ ID NO:3815, SEQ ID NO:3817, SEQ ID NO:3819, SEQ ID NO:3821, SEQ ID NO:3823, SEQ ID NO:3825, SEQ ID NO:3827, SEQ ID NO:3829, SEQ ID NO:3831, SEQ ID NO:3833, SEQ ID NO:3835, SEQ ID NO:3837, SEQ ID NO:3839, SEQ ID NO:3841, SEQ ID NO:3843, SEQ ID NO:3845, SEQ ID NO:3847, SEQ ID NO:3849, SEQ ID NO:3853, SEQ ID NO:3855, SEQ ID NO:3857, SEQ ID NO:3859, SEQ ID NO:3861, SEQ ID NO:3863, SEQ ID NO:3865, SEQ ID NO:3867, SEQ ID NO:3869, SEQ ID NO:3871, SEQ ID NO:3873, SEQ ID NO:3875, SEQ ID NO:3877, SEQ ID NO:3879, SEQ ID NO:3881, SEQ ID NO:3883, SEQ ID NO:3885, SEQ ID NO:3887, SEQ ID NO:3889, SEQ ID NO:3891, SEQ ID NO:3893, SEQ ID NO:3895, SEQ ID NO:3897, SEQ ID NO:3899, SEQ ID NO:3901, SEQ ID NO:3903, SEQ ID NO:3905, SEQ ID NO:3907, SEQ ID NO:3909, SEQ ID NO:3911, SEQ ID NO:3913, SEQ ID NO:3915, SEQ ID NO:3917, SEQ ID NO:3919, SEQ ID NO:3921, SEQ ID NO:3923, SEQ ID NO:3925, SEQ ID NO:3927, SEQ ID NO:3929, SEQ ID NO:3931, SEQ ID NO:3933, SEQ ID NO:3935, SEQ ID NO:3937, SEQ ID NO:3939, SEQ ID NO:3941, SEQ ID NO:3943, SEQ ID NO:3945, SEQ ID NO:3947, SEQ ID NO:3949, SEQ ID NO:3951, SEQ ID NO:3953, SEQ ID NO:3955, SEQ ID NO:3957, SEQ ID NO:3959, SEQ ID NO:3961, SEQ ID NO:3963, SEQ ID NO:3967, SEQ ID NO:3969, SEQ ID NO:3971, SEQ ID NO:3973, SEQ ID NO:3975, SEQ ID NO:3978, SEQ ID NO:3980, SEQ ID NO:3982, SEQ ID NO:3984, SEQ ID NO:3986, SEQ ID NO:3989, SEQ ID NO:3991, SEQ ID NO:3993, SEQ ID NO:3995, SEQ ID NO:3997, SEQ ID NO:3999, SEQ ID NO:4002, SEQ ID NO:4005, SEQ ID NO:4007, SEQ ID NO:4009, SEQ ID NO:4011, SEQ ID NO:4013, SEQ ID NO:4017, SEQ ID NO:4019, SEQ ID NO:4021 SEQ ID NO:4023, SEQ ID NO:4025, SEQ ID NO:4027, SEQ ID NO:4029, SEQ ID NO:4031, SEQ ID NO:4033, SEQ ID NO:4035, SEQ ID NO:4037, SEQ ID NO:4039, SEQ ID NO:4041, SEQ ID NO:4043, SEQ ID NO:4045, SEQ ID NO:4047, SEQ ID NO:4049, SEQ ID NO:4051, SEQ ID NO:4053, SEQ ID NO:4055, SEQ ID NO:4057, SEQ ID NO:4059, SEQ ID NO:4061, SEQ ID NO:4063, SEQ ID NO:4065, SEQ ID NO:4067, SEQ ID NO:4069, SEQ ID NO:4071, SEQ ID NO:4073, SEQ ID NO:4075, SEQ ID NO:4077
SEQ ID NO:4079, SEQ ID NO:4081, SEQ ID NO:4083, SEQ ID NO:4085, SEQ ID NO:4087, SEQ ID NO:4089, SEQ ID NO:4091, SEQ ID NO:4093, SEQ ID NO:4095, SEQ ID NO:4097, SEQ ID NO:4100, SEQ ID NO:4102, SEQ ID NO:4104, SEQ ID NO:4106, SEQ ID NO:4108, SEQ ID NO:4110, SEQ ID NO:4112, SEQ ID NO:4114, SEQ ID NO:4116, SEQ ID NO:4118, SEQ ID NO:4120, SEQ ID NO:4122, SEQ ID NO:4124, SEQ ID NO:4126, SEQ ID NO:4128, SEQ ID NO:4130, SEQ ID NO:4133, SEQ ID NO:4135, SEQ ID NO:4138, SEQ ID NO:4141, SEQ ID NO:4143, SEQ ID NO:4145, SEQ ID NO:4147, SEQ ID NO:4149, SEQ ID NO:4151, SEQ ID NO:4153, SEQ ID NO:4156, SEQ ID NO:4158, SEQ ID NO:4160, SEQ ID NO:4162,

SEQ ID NO:4164, SEQ ID NO:4166
SEQ ID NO:4169, SEQ ID NO:4171, SEQ ID NO:4173, SEQ ID NO:4175, SEQ ID NO:4177, and SEQ ID NO:4179

(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences of (b);
(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);
(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);
(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence of (a).

9. A substantially pure protein encoded by the polynucleotide of claim 8.

10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.

11. A vector comprising the polynucleotide of claim 5 or 8.

12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.

15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.

16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.

17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.

18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.

19. A method for synthesizing a polynucleotide, the method comprising:

a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
b) recovering the synthesized product.

20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.

21. The method of claim 19, wherein the complementary strand is obtainable by PCR.

22. A method for detecting the polynucleotide of claim 8, the method comprising:

a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.

23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium

on which the database is stored.

Figure 1

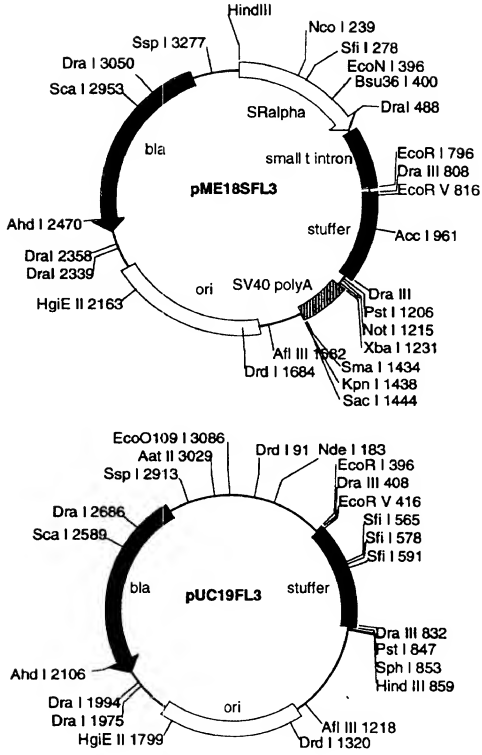

HindIII
Nco I 239
Sfi I 278
EcoN I 396
Bsu36 I 400
DraI 488
SRalpha
small t intron
EcoR I 796
Dra III 808
EcoR V 816
Acc I 961
stuffer
SV40 polyA
Dra III
Pst I 1206
Not I 1215
Xba I 1231
Sma I 1434
Kpn I 1438
Sac I 1444
AflIII 1662
Drd I 1684
ori
HgiE II 2163
DraI 2339
DraI 2358
Ahd I 2470
bla
Sca I 2953
Dra I 3050
Ssp I 3277
pME18SFL3
EcoO109 I 3086
Aat II 3029
Ssp I 2913
Dra I 2686
Sca I 2589
Drd I 91
Nde I 183
EcoR I 396
Dra III 408
EcoR V 416
Sfi I 565
Sfi I 578
Sfi I 591
stuffer
Dra III 832
Pst I 847
Sph I 853
Hind III 859
AflIII 1218
Drd I 1320
ori
HgiE II 1799
Dra I 1975
Dra I 1994
Ahd I 2106
bla
pUC19FL3

Figure 2

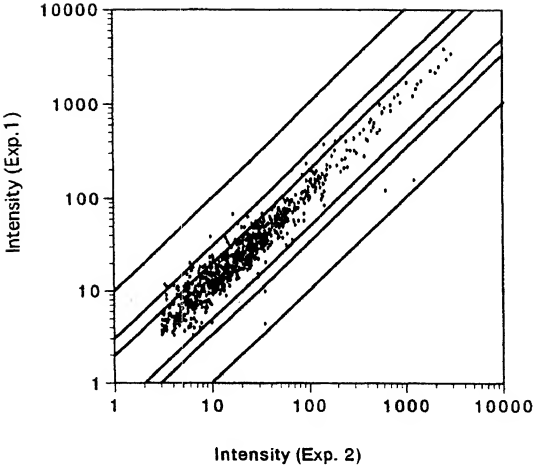
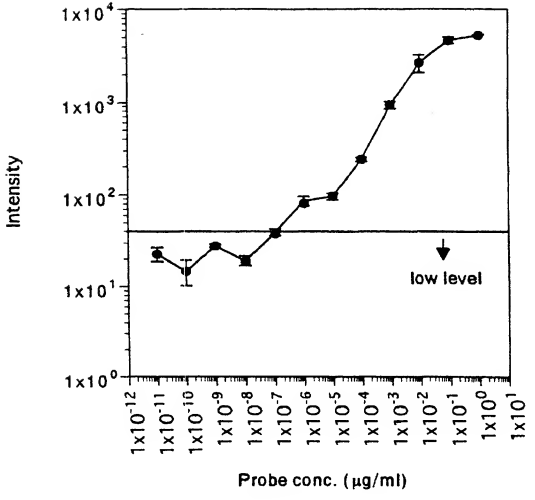

10000
1000
100
10
1
Intensity (Exp.1)
1
10
100
1000
10000
Intensity (Exp. 2)

Figure 3


Intensity
1x10^4
1x10^3
1x10^2
1x10^1
1x10^0
low level
1x10^-12
1x10^-11
1x10^-10
1x10^-9
1x10^-8
1x10^-7
1x10^-6
1x10^-5
1x10^-4
1x10^-3
1x10^-2
1x10^-1
1x10^0
1x10^1
Probe conc. (µg/ml)

Identifier:	AAK94459 cDNA Sequence 2535 BP
Release Info:	Derwent Geneseq Database Release No. 200124; Date released 26-NOV-01
Database XReference:	WPI; 2001-524255/58.;P-PSDB; AAM93529.
Accession Number:	AAK94459
Patent Title:	830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation -
Patented by:	(HELI-) HELIX RES INST.
Inventor:	Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H
Description:	Human full-length cDNA, SEQ ID NO: 3266.
Patent Number:	EP1130094-A2
Patent Publication Date:	05-SEP-2001
Modification Date:	06-NOV-2001 (first entry)
Local Filing:	07-JUL-2000; 2000EP-0114089
Priority:	08-JUL-1999
Abstract:	The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
KeyWords:	Human;full length cDNA;cDNA synthesis;oligo-capping;ss.
Organism	Homo sapiens.
Sequence Composition:	Sequence 2535 BP; 482 A; 807 C; 871 G; 375 T; 0 other;
Sequence:	>AAK94459 EP1130094-A2 PA (HELI-) HELIX PR 08-JUL-1999 PF 07-JUL-2000 Human full-length cDNA, SEQ ID NO: 3266. [Homo sapiens.]

GAGAGCCTGAGCAGGCAGGGCACCTCCAGGTGGGCAGGAGCTACCACTCAGCACCATGAG
CACCGCCACAGGCCCAGAAGCTGCCCCAAAGCCAAGCGCCAAGTCTATCTATGAGCAGAG
GAAGCGTTACTCCACAGTTGTTACGGCTGATGTATCCCAGTACCCAGTCAATCACCTGGT
GACGTTCTGCCTGGGTGAGGACGATGGCGTGCATACCGTGGAGGATGCCTCCAGGAAGTT
GGCCGTCATGGATAGCCAGGGCCGAGTCTGGGCACAGGAGATGCTGCTGCGAGTGTCTCC
CGACCATGTCACGCTGCTCGACCCGGCCTCCAAGGAGGAGCTGGAGTCGTACCCACTGGG
CGCCATCGTGCGCTGTGACGCGGTGATGCCACCCGGCAGGAGCCGCTCGTTGCTGCTGCT
CGTGTGCCAGGAACCCGAGCGCGCGCAGCCCGACGTGCACTTCTTCCAGGGCCTGCGCCT
CGGGGCGGAGCTGATCCGAGAGGACATCCAGGGGGCTCTGCACAATTACCGCTCGGGCCG
CGGGGAGCGCAGGGCGGCGGCGCTCAGGGCCACGCAGGAGGAGTTGCAGCGCGACCGCTC
GCCCGCCGCTGAGACCCCGCCCCTGCAGCGCCGCCCGTCAGTCCGCGCAGTGATCAGCAC
CGTAGAGCGGGGCGCGGGCCGCGGACGACCCCAGGCGAAGCCCATTCCCGAGGCAGAGGA
GGCGCAGAGGCCTGAGCCGGTGGGGACCTCGAGCAACGCTGACTCGGCCTCCCCGGACCT
GGGTCCCCGGGGTCCTGACCTGGCGGTTCTGCAGGCGGAGCGGGAAGTGGACATCCTGAA
CCACGTGTTCGACGACGTAGAGAGCTTTGTATCGAGGCTGCAGAAGTCGGCGGAGGCGGC
CAGGGTGCTGGAGCACCGGGAACGCGGCCGCAGGAGCCGGCGCCGGGCGGCTGGGGAGGG
CTTGCTGACGCTGCGGGCCAAGCCGCCCTCGGAGGCCGAGTACACCGACGTGCTGCAGAA
GATCAAGTACGCCTTCAGCCTGCTGGCCCGGCTGCGCGGCAACATCGCCGACCCCTCCTC
TCCGGAGCTGTTGCACTTCCTTTTCGGGCCTCTGCAGATGATTGTGAACACGTCGGGGGG
GCCGGAGTTCGCGAGCAGTGTGCGGCGGCCGCATCTGACATCGGATGCCGTGGCGCTGCT
GCGGGACAACGTCACTCCACGTGAAAACGAGCTCTGGACCTCGCTGGGGGACTCGTGGAC

CCGCCCCGGGCTGGAGCTGTCCCCGGAGGAGGGACCCCCATACAGACCCGAGTTCTTCAG
CGGCTGGGAGCCGCCGGTCACTGACCCGCAGAGCCGCGCCTGGGAGGACCCAGTTGAGAA
ACAGCTACAGCACGAGCGGAGGCGCCGGCAGCAAAGCGCCCCCCAGGTCGCTGTCAATGG
TCACCGAGACTTGGAGCCAGAATCTGAGCCTCAGCTGGAGTCAGAGACAGCAGGAAAATG
GGTCCTGTGTAATTATGACTTCCAGGCCCGCAACAGCAGTGAGCTGTCGGTCAAGCAGCG
GGACGTACTGGAGGTCCTGGATGACAGTCGTAAGTGGTGGAAGGTTCGGGACCCAGCGGG
GCAGGAGGGATATGTGCCCTACAACATCCTGACACCCTACCCCGGACCCCGGCTGCACCA
CAGCCAAAGCCCTGCCCGCAGCCTGAACAGCACTCCTCCTCCACCACCAGCCCCAGCCCC
GGCCCCACCTCCAGCTCTGGCTCGGCCCCGCTGGGACAGGCCCCGCTGGGACAGCTGCGA
TAGCCTCAACGGCTTGGACCCCAGCGAGAAGGAGAAATTCTCCCAGATGCTCATCGTCAA
CGAGGAACTGCAGGCGCGCCTGGCCCAGGGCCGCTCGGGACCGAGCCGCGCAGTCCCAGG
GCCCCGCGCCCCGGAACCGCAGCTCAGCCCGGGCTCGGACGCCTCCGAGGTCCGCGCCTG
GCTGCAGGCCAAGGGCTTTAGCTCCGGGACCGTGGACGCGCTGGGTGTGCTGACCGGGGC
GCAGCTTTTCTCGCTGCAGAGGGAGGAGCTGCGGGCGGTGAGCCCCGAGGAGGGGGCACG
TGTGTACAGCCAGGTCACCGTGCAGCGCTCGCTGCTGGGGGACAAAGAGAAAGTGTCAGA
GCTGGAGGCAGTGATGGAGAAGCAAAAGAAGAAGGTGGAAGGCGAGGTGGAAATGGAGGT
CATTTGACCTGCCAGGCGCCCTTCGCAAAGAGTGACGAGGCCCCGTGGGAGAACGGACTC
CTCAGACTCTCCCCAATAGCGGAAGTCGATCTTCTGAAGGATGGCCAATCTGCTCCGGCC
CTGGTCTTCCCCCATCCCGGTGGACAGACTTAACGATCCTTGCTGCAGTCCCTCCGGAGA
GGATCTGGACTGGCTGGGAGTGGGGAGGGCGTGGAGACAGTCTACGGAAAGCGCTAGCAG
ACCCCCGAGAGGGTGCAGTGGAGCCCTGAGCATTGTAATATGCGGCCCAGCCTATAAACA
GCCTCCGTGCTTAGC